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No.	Doccode	Number of pages
1	SRNT	110

Total number of pages: 110

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A DOCPHOENIX

# APPL PARTS

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 \_\_\_\_\_ SPEC NO \_\_\_\_\_  
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 \_\_\_\_\_ NFDR \_\_\_\_\_  
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\_\_\_\_\_ CTMS \_\_\_\_\_  
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# INCOMING

\_\_\_\_\_ AP.B \_\_\_\_\_  
 Appeal Brief  
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 Change of Address  
 \_\_\_\_\_ N/AP \_\_\_\_\_  
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 Change in Power of Attorney  
 \_\_\_\_\_ REM \_\_\_\_\_  
 Applicant Remarks in Amendment  
 \_\_\_\_\_ XT/ \_\_\_\_\_  
 Extension of Time filed separate

## Internal

03-05-83 SRNT 100  
 Examiner Search Notes  
 \_\_\_\_\_ CLMPTO \_\_\_\_\_  
 PTO Prepared Complete Claim Set

\_\_\_\_\_ ECBOX \_\_\_\_\_  
 Evidence Copy Box Identification  
 \_\_\_\_\_ WCLM \_\_\_\_\_  
 Claim Worksheet  
 \_\_\_\_\_ WFEE \_\_\_\_\_  
 Fee Worksheet

## File Wrapper

\_\_\_\_\_ FWCLM \_\_\_\_\_  
 File Wrapper Claim  
 \_\_\_\_\_ IIFW \_\_\_\_\_  
 File Wrapper Issue Information  
 \_\_\_\_\_ SRFW \_\_\_\_\_  
 File Wrapper Search Info





**SEARCH REQUEST FORM**

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
 Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
 Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

**If more than one search is submitted, please prioritize searches in order of need.**

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STANDARD FORM NO. 64  
 5010-104  
 (Rev. 1-78)

\*\*\*\*\*  
**STAFF USE ONLY**

	Type of Search	Vendors and cost where applicable
Searcher _____	NA Sequence (#) _____	STN _____
Searcher Phone # _____	AA Sequence (#) <input checked="" type="checkbox"/> _____	Dialog _____
Searcher Location _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up _____	Bibliographic _____	Dr Link _____
Date Completed _____	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time _____	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/> _____
Clerical Prep Time _____	Patent Family _____	WWW/Internet _____
Online Time _____	Other _____	Other (specify) _____



GenCore version 5.1.3  
Copyright 1993-2003 Compugen Ltd

10M protein - protein search, using sw model

Run on: March 5, 2003, 08:10: Search time 46 seconds  
(without alignments)  
8,360 Million cell updates/sec

Title: US-09-732 411 15

Perfect score: 20

Sequences: 1 VLEP 4

Scoring table: BLOSUM62

Gapop 10 0 0 Gapext 0 5

Searched: 283224 seqs, 96134420 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database: PIR 73.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	20	100.0	28	2 A27261	proteinase inhibitor
2	20	100.0	37	2 G28927	protein p10 - curl
3	20	100.0	58	2 S03810	beta1 protein - Rhi
4	20	100.0	59	2 R60212	T-cell surface gly
5	20	100.0	59	2 AC1286	LSU ribosomal prot
6	20	100.0	61	2 T03065	cytochrome c oxida
7	20	100.0	62	2 C90471	hypothetical prote
8	20	100.0	63	2 F89902	hypothetical prote
9	20	100.0	64	2 C44484	hypothetical prote
10	20	100.0	77	2 C73268	hypothetical prote
11	20	100.0	80	2 T15296	hypothetical prote
12	20	100.0	81	2 F80154	hypothetical prote
13	20	100.0	92	2 T42093	hypothetical prote
14	20	100.0	93	2 T19717	hypothetical prote
15	20	100.0	86	2 C69107	hypothetical prote
16	20	100.0	89	2 E73296	hypothetical prote
17	20	100.0	92	2 T80349	plastoquinol-plast
18	20	100.0	93	2 B86755	prophage p12 prote
19	20	100.0	93	2 AF0923	peptidyl-prolyl ci
20	20	100.0	93	2 F91217	peptidylprolyl iso
21	20	100.0	93	2 F86062	peptidylprolyl iso
22	20	100.0	93	2 S48658	peptidylprolyl iso
23	20	100.0	99	2 T37093	hypothetical prote
24	20	100.0	101	2 T25656	hypothetical prote
25	20	100.0	102	2 C52711	probable neurosept
26	20	100.0	103	2 F86564	yidd family [impor
27	20	100.0	103	2 H72060	yidd family [Chla
28	20	100.0	105	1 P4MXP	ribosomal protein
29	20	100.0	105	2 S04150	plastoquinol-plast

30	20	100.0	105	2 AE1848	hypothetical prote
31	20	100.0	105	2 S76770	hypothetical prote
32	20	100.0	106	2 F81506	hypothetical prote
33	20	100.0	108	2 T13133	protein gp46 - pla
34	20	100.0	108	2 T41447	very hypothetical
35	20	100.0	109	2 F70677	hypothetical prote
36	20	100.0	111	2 D72112	hypothetical prote
37	20	100.0	111	2 F85511	hypothetical prote
38	20	100.0	112	2 B69438	hypothetical prote
39	20	100.0	113	2 T30436	hypothetical prote
40	20	100.0	113	2 F90119	hypothetical prote
41	20	100.0	114	2 H87113	nitrogen regulator
42	20	100.0	115	2 F72716	hypothetical prote
43	20	100.0	115	2 G83426	hypothetical prote
44	20	100.0	116	1 QOPSHT	hypothetical prote
45	20	100.0	116	1 QC2BHT	hypothetical prote
46	20	100.0	116	2 F80673	merit protein, 12
47	20	100.0	116	2 B33858	merit protein - Eac
48	20	100.0	116	2 S70142	merit protein - Eac
49	20	100.0	116	2 H96643	hypothetical prote
50	20	100.0	117	2 L69335	carboxylate dehydrat

ALIGNMENTS

RESULT 1

A27261

proteinase inhibitor 3 - sea anemone (Stichodactyla sp.) (fragments)

C.Species: Stichodactyla sp., Stichodactyla sp.

C.Date: 31-Mar-1998 #sequence\_revision 31-Mar-1998 #text\_change 18-Jun-1998

C.Accession: A27261

R.Mebs, D.; Gebauer, E.

Toxicol 20: 335, 1982

A.Title: Structural studies on a proteinase inhibitor from the sea anemone Stichodactyla sp.

A.Preference number: A27261

A.Accession: A27261

A.Molecule type: protein

A.Residues: 1-28 <MEB>

Query Match 100.0%; Score 20; DB 2; Length 28;

Best Local Similarity 100.0%; Pred. No. 81;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4

DB 4 VLEP 7

RESULT 2

G28027

protein p10 - curled (leaved tobacco) (fragment)

C.Species: Nicotiana glauca (leaved tobacco)

C.Date: 19-MAY-1989 #sequence\_revision 13 May 1989 #text\_change 11 Jun 1989

C.Accession: G28027

P.Ram, G.; De Looze, M.; Inze, D.; Van Montagu, M.; Van Deckerckhove, J.

Proc Natl Acad Sci U S A 84: 4806-4810, 1987

A.Title: Alterations in the phenotype of plant cells studied by NMR terminal amino acid

A.Preference number: A94167

A.Accession: G28027

A.Molecule type: protein

A.Residues: 1-37 <BAU>

C.Superfamily: thaumatin 1

Query Match 100.0%; Score 20; DB 2; Length 37;

Best Local Similarity 100.0%; Pred. No. 114-02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4

DB 29 VLEP 32

### RESULT 3

S03810  
 pss1 protein - Rhizobium leguminosarum bv. phaseoli  
 C.Species: Rhizobium leguminosarum bv. phaseoli  
 C.Date: 29 Feb 1990 #sequence\_revision 28 Feb 1990 #text\_change 11-Jan-2000  
 C.Accession: S03810  
 R.Borthakur, D.; Barker, P. F.; Iatchford, J. W.; Pessen, L.; Johnston, A. W.B.  
 Mol. Gen. Genet. 213, 155-162, 1988  
 A>Title: Analysis of pss genes of Rhizobium leguminosarum required for exopolysaccharide  
 genes.  
 A.Reference number: S03810, NCID:89427136, FMD:2851702  
 A.Accession: S03810  
 A.Molecule type: DNA  
 A.Residues: 1-58 <BOR>  
 A.Cross-References EXP: X12558, NID:347355, PIDN CAAL078.1, PID 346256  
 C.Genetics:  
 A:Gene: pss1  
 C:Superfamily: Aquifex aeolicus cysO protein

```

Query Match      100.0%   Score 20, DB 2, Length 58;
Best Local Similarity 100%   Eval No 1, E-300;
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY      1 VLER 4
        ||||
db       54 VLEP 57

```

## RESULT 4

Accession: B60232  
Molecule type: mRNA  
A.PesResidues: 1-59 <OLE>  
A.PesReferences: GP\_X53359, NID\_9387745, FIRM\_PAA33357.1, PDB\_3J8774C  
A.Superfamily: T-cell surface glycoprotein CD3 delta chain; immunoglobulin homology domain; alpha chain; transmembrane protein

Cody Mach	100%	Sore	100%	Lynch
Besse Leger	100%	Erd Mc	100%	
Mattalag	Conservative	O. Vignatone		Travis
QY	1 VLEP 4			
b6	26 VLEP 29			

## RESULTS

LSU ribosomal protein L32P [imported] - Brucella melitensis (strain 16M)  
Accession: AC1286  
Species: Brucella melitensis  
CDate: 01-Feb-2002 #sequence revision: 01-Feb-2002 #text change: 17-May 2002  
CAccession: AC1286  
RefVecBioInfo: V.G. Kaparal, V.I. Podkat, P.J. Patra, G.L. Miller, S. Ios, T. Ivanova,  
F. Mazur, M.G. Goldman, E. Salukow, E. Elzer, P.H. Hagens, S. O'Callaghan, D. Letessier,  
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A>Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
A:Reference number: AD352; PMID:11756688  
A:Accession: AC1286  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 159 kbp  
A:Accession: AC1286  
A:Experimental source: strain 16M  
A:Genetics:  
A:Gene: EXE1286

A;Map position: I  
C:Superfamily: Escherichia coli ribosomal protein L32

```
Query Match      100.0%, Score 20, DB 2: Length 59;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches      4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

## RESULT 6

T03065  
cytochrome c oxidase homolog O41L - Chilo iridescent virus  
C/Species: Chilo iridescent virus  
C/Date: 24-Mar-1999 #sequence revision 24-Mar 1999 #ext\_change 02-Oct-1999  
C/Accession: T03065  
R/Bahr, U.; Tidona, C.A.; Darai, G.  
Virus Genes 15, 225-245, 1997  
A/Title: The RNA sequence of Chilo iridescent virus between the genome and  
A/Reference: 104834, MN1981160, MN19492589  
A/Accession: T03065  
A/Status: preliminary; translated from GE/EMBL/DBDU  
A/Molecule type: DNA  
A/Residues: 1-61 <BAH>  
A/Cross-references: EMBL AF002334; NID:Q573835, PID:AA094439.1; PID:Q573838

```

Query Match      100.0%, Score 20, DB 2, Length 61;
Best Local Similarity 100.0%; Pred No. 1 9e.02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

## RESULT 7

CQ0471  
 hypothetical protein SS01456 [imported] - Sulfolobus solfataricus transposon ISG1058  
 CSpecies: Sulfolobus solfataricus  
 CDate 24 May 2001 #sequence\_revision 24 May 2001 #text\_change 24 May 2001  
 CAccession: CQ0471  
 PSto, G. Jeffery, P. F. Confalonieri, P. Litvinov, Y. Allard, G. Axayev, M. J. Chan, W.  
 Cheng, I. J. Drenth, A. E. Fierste, C. W. Miller, H. Puch, X. Zhang, H. P. Redder, P.  
 Strobel, A. Szilagyi, M. A. Sussner, C. W. Van der Oost, J.  
 submitted to GenBank, April 2001  
 ADescription: Sulfolobus solfataricus, a filamentous bacterium.  
 AReference number: A99139

[illegible]

RESULT 8

R59801 8  
 E98802  
 hypotetical protein [imported] - Staphylococcus aureus (strain N315)  
 Species: Staphylococcus aureus  
 C.Date: 10 May 2001 #Sequence\_revision is May-2001 #rev\_change 00-000- 2001  
 C.Accession: E98802  
 E.Furuta, M. Kita, T. Teshiyama, I. Baba, T. Kuwano, H. Kobayashi, I.

[illegible]

ma, A.; Mizutani, M.; Y. Kobayashi, N.; Sawan, T.; Inoue, P.; Fatio, G.; Sekimizu, K.;  
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
Lancet 357, 1235-1240, 2001.  
A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.  
A:Reference number: A84748; MUID-21311952; PMID:11418146  
A:Accession: E89802  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-63 <KUR>  
A:Cross-references: GR:BA000018, PID:313700078, PID:BA011576 1; GSPRP:G800149  
A:Experimental source: strain N315  
A:Genetics:  
A:Gene: SAS009

Query Match 100.0% Score 20; DB 2; Length 63;  
Best Local Similarity 100.0% Pred No. 2; 0; 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QV 1 VLEP 4  
DB 35 VLEP 38

RESULT 9  
G84484  
hypothetical protein At2g07350 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Feb-2001 #sequence\_revision 02 Feb 2001 #ext\_change 02-Feb-2001  
C:Accession: G84484  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID-20083487; PMID:10617197  
A:Accession: G84484  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-68 <STO>  
A:Cross-references: GR:AF000091, MUID:3430078, PID:MA01607 1; GSPRP:G800130  
A:Genetics:  
A:Gene: At2g07350  
A:Map position: 2

Query Match 100.0% Score 20; DB 2; Length 68;  
Best Local Similarity 100.0% Pred No. 2; 0; 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QV 1 VLEP 4  
DB 6 VLEP 9

RESULT 10  
C72645  
hypothetical protein APES025 - Aeropyrum pernix (strain P1)  
C:Species: Aeropyrum pernix  
C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #ext\_change 20-Aug-1999  
C:Accession: C72645  
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix.  
A:Reference number: A72450; MUID-0931030; PMID:10392966  
A:Accession: C72645  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-77 <KAW>  
A:Cross-references: GR:AP000000; MUID:AP000000; PID:G5104188; PID:BA079563 1; PID:di043349; PID:G510742003  
A:Experimental source: strain K1  
A:Genetics:  
A:Gene: APES025

Query Match 100.0% Score 20; DB 2; Length 68;  
Best Local Similarity 100.0% Pred No. 2; 0; 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QV 1 VLEP 4  
DB 6 VLEP 9

RESULT 11  
T15286  
hypothetical protein M01D7.5 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #ext\_change 20-Sep-1999  
C:Accession: T15286  
A:Title: The sequence of *C. elegans* cosmid M01D7.  
A:Reference number: Z18322  
A:Accession: T15286  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-80 <GAT>  
A:Cross-references: EMBL:AF003730; MUID:32105482; PID:32105484; PID:AA048666 1; GSPRP:G800107  
A:Experimental source: strain Bristol N2, clone M01D7  
A:Genetics:  
A:Gene: CESP:M01D7.5  
A:Map position: 1  
A:Transons: 19/1; 38/3

Query Match 100.0% Score 20; DB 2; Length 80;  
Best Local Similarity 100.0% Pred No. 2; 0; 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QV 1 VLEP 4  
DB 72 VLEP 75

RESULT 12  
E90324  
hypothetical protein SSC8568 [imported] - Sulfolobus solfataricus transposon IS1129  
C:Species: Sulfolobus solfataricus  
C:Date: 24-May-2001 #sequence\_revision 24-May-2001 #ext\_change 24-May-2001  
C:Accession: E90324  
A:Title: Sulfolobus solfataricus transposon IS1129.  
A:Reference number: A99139  
A:Accession: E90324  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-81 <KUR>  
A:Cross-references: GR:AE000641, MUID:319814884, PID:AA04182 1; GSPRP:G800104  
A:Genetics:  
A:Gene: SSC8568

Query Match 100.0% Score 23; DB 2; Length 81;  
Best Local Similarity 100.0% Pred No. 2; 0; 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QV 1 VLEP 4  
DB 23 VLEP 26

RESULT 13  
742003  
hypothetical protein H3 - human herpesvirus 7 (strain J1)  
C:Species: human herpesvirus 7  
A:Variety: strain J1

[illegible]



A:Title: Confirmation of the existence of a third family among peptidyl-prolyl cis/trans  
 A:Reference number: S48658; PMID:8401874, PMID:7925971  
 A:Accession: S48658  
 A:Molecule type: DNA  
 A:Residues: 1-93 <RAH>  
 A:Cross-references: GR 231874, MID:G613730, PIRN:AAR32064 1, PID:3693900  
 R:Rahfeld, J.; Buchkragel, K.F.; Schelbert, B.; Ludwig, B.; Hacker, J.; Mann, K.; Fischer,  
 submitted to the Protein Sequence Database, August 1994  
 A:Description: Confirmation of the existence of a third family among peptidyl-prolyl cis  
 A:Reference number: S45525  
 A:Accession: S45525  
 A:Molecule type: protein  
 A:Residues: 2-93 <RAH>  
 A:Experimental source: strain K-12  
 R:Rahfeld, J.U.; Schierhorn, A.; Mann, K.; Fischer, G.  
 FEBS Lett. 343, 65-69, 1994  
 A:Title: A novel peptidyl-prolyl cis/trans isomerase from Escherichia coli.  
 A:Reference number: S43654; PMID 94215700, PMID 8163020  
 A:Accession: S43654  
 A:Molecule type: protein  
 A:Residues: 2-22 <RAH>  
 A:Experimental source: strain K-12  
 R:Rahfeld, J.U.; Plattett, F.P.; Plattett, F.; G.; Bloch, C.A.; Perna, N.T.; Parland, V.; Piloy, M.; Co  
 A.; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A:Title: The complete genome sequence of Escherichia coli K-12.  
 A:Reference number: A4720; MID:9426617, PMID 9278503  
 A:Accession: B65181  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-93 <BLAT>  
 A:Cross-references: GR A4720; MID:9426617, PMID 9278503  
 A:Experimental source: strain K-12, substrain MG1655  
 C:Genetics:  
 A:Gene: ppvC  
 C:Keywords: cis-trans-isomerase; cyclosporin A binding

Query Match 100.0%; Score 20; DB 2; Length 92;  
 Best Local Similarity 100.0%; Pred No 3 1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLEP 4  
 Db 71 VLEP 74

RESULT 23  
 T37093  
 hypothetical protein SCJ4.10 - Streptomyces coelicolor  
 C:Species: Streptomyces coelicolor  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
 C:Accession: T37093  
 R:Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.  
 submitted to the EMBL Data Library, August 1999  
 A:Reference number: Z21588  
 A:Accession: T37093  
 A:Status: preliminary, translated from GB/EMBL/SDSJ  
 A:Molecule type: DNA  
 A:Residues: 1-99 <SAU>  
 A:Cross-references: FMBL A110200, PIDN CAB2244 1, GSPTC:GN00070, S00EDB:SCJ4.10  
 A:Experimental source: strain A3(2)  
 C:Genetics:  
 A:Gene: SCCEDB:SCJ4 10

Query Match 100.0%; Score 20; DB 2; Length 99;  
 Best Local Similarity 100.0%; Pred No 3 3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLEP 4  
 Db 22 VLEP 25

RESULT 24  
 T25656  
 hypothetical protein CS3C11.4 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
 C:Accession: T25656  
 R:Du, Z  
 submitted to the EMBL Data Library, February 1997  
 A:Description: The sequence of C. elegans cosmid c53C11  
 A:Reference number: Z20064  
 A:Accession: T25656  
 A:Status: preliminary; translated from GB/EMBL/DNBJ  
 A:Molecule type: DNA  
 A:Residues: 1-101 <NUZ>  
 A:Cross-references: EMBL U98192, PIDN AAB42309 1, GSPTC:GN00020, GESP:CS3C11.4  
 A:Experimental source: strain Bristol N2; clone CS3C11  
 C:Genetics:  
 A:Gene: GESP-CS3C11.4  
 A:Map position: X

Query Match 100.0%; Score 20; DB 2; Length 101;  
 Best Local Similarity 100.0%; Pred No 3 4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLEP 4  
 Db 15 VLEP 18

RESULT 25  
 S52711  
 probable neuropeptide precursor HDS2 - Helix lucorum  
 C:Species: Helix lucorum  
 C:Date: 19-Mar 1997 #sequence\_revision 19-Mar-1997 #text\_change 05-Nov-1999  
 C:Accession: S52711  
 R:Bogdanov, Y.D.; Balaban, P.M.; Belyavsky, A.V.  
 submitted to the EMBL Data Library, March 1995  
 A:Description: Two novel genes are specifically expressed in D-group neurons of the ter  
 A:Reference number: S52710  
 A:Accession: S52711  
 A:Molecule type: mRNA  
 A:Residues: 1-102 <BOG>  
 A:Cross-references: EMBL X85749, MID:9755751, PIRN:CAAE0751 1, PIP:3755752  
 A:Experimental source: tissue type nervous ganglia  
 C:Genetics:  
 A:Gene: HDS2

Query Match 100.0%; Score 20; DB 2; Length 102;  
 Best Local Similarity 100.0%; Pred No 3 5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLEP 4  
 Db 46 VLEP 49

Search completed: March 5, 2003, 08:34:15  
 Job time : 48 secs



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OM protein - protein search, using sw model

Run on: Match: 5, 2033, on 27 14, Search time 25 seconds  
(without alignments)  
5 721 Million cell updates/sec

Title: US-09-732-411-15

Perfect score: 20

Sequence: 1 VLEP 4

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112992 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	59	CD3D_BOVIN	Q28072 bos taurus
2	20	100.0	59	PL32_BPME	Q8YJ14 bruceella m
3	20	100.0	71	IFI_EPIN	Q9X214 leptoosira
4	20	100.0	92	PPIC_FCOLI	P9159 escherichia
5	20	100.0	95	PPIC_SALTY	Q6L63 salmonella
6	20	100.0	95	YESS_RHILP	P1G497 thizobium l
7	20	100.0	98	FP02_TBEAQ	Q36V4 thermus aqu
8	20	100.0	100	V62_EPR01	Q37866 bacteriophi
9	20	100.0	103	Y592_CHLPH	Q429W2 chlamydia p
10	20	100.0	105	PL3F_METVA	P14025 methanococ
11	20	100.0	106	PTD_HOPVJ	P12361 hordeum vul
12	20	100.0	112	YF07_ACFU	Q28765 archaeoglob
13	20	100.0	114	RLA2_EIMTE	Q967Y9 eimeria ten
14	20	100.0	116	MEPT_AICCA	Q62106 acinetobact
15	20	100.0	116	MEPT_ALGSP	P44185 alcaligenes
16	20	100.0	116	MERT_PSEAF	Q91440 pseudomonas
17	20	100.0	116	MEPT_PSEFL	Q91769 pseudomonas
18	20	100.0	116	MEPT_SALTI	P04336 salmonella
19	20	100.0	116	MEPT_SEPMA	P13112 serotatia ma
20	20	100.0	116	PEV_HV10Y	P20887 human immun
21	20	100.0	117	DHS0_ACFU	Q29873 archaeoglob
22	20	100.0	120	SYE_STAXY	P77984 staphylococ
23	20	100.0	126	MEPT_ENTAG	P44700 enterobacte
24	20	100.0	129	UMPL_SCHPO	Q74416 schizosacch
25	20	100.0	129	V101_YEAST	P40461 saccharomyc
26	20	100.0	134	WN11_CHICK	Q91029 gallus gall
27	20	100.0	136	PK16_MAIZE	P08528 zea mays am
28	20	100.0	139	PETD_PEA	P06527 pisum sativ
29	20	100.0	146	YH51_YEAST	P40342 saccharomyc
30	20	100.0	147	V336_HSV1	Q00146 ictulurid h
31	20	100.0	153	LEX1_MOUSE	P46694 mus musculu
32	20	100.0	156	LEX1_HUMAN	P46695 homo sapien
33	20	100.0	157	HEP2_MOUSE	Q54722 mus muscul

34	20	100.0	157	1	HES2_RAT	P35429 rattus norv
35	20	100.0	158	1	VH21_MYXVL	P09460 myxoma viru
36	20	100.0	160	1	PETD_ARATH	P06774 arabidopsis
37	20	100.0	160	1	PETD_MAIZE	P06643 zea mays am
38	20	100.0	160	1	PETD_MAPPO	P06750 marchantia
39	20	100.0	163	1	PETD_MESVI	Q9M972 mesocriceta
40	20	100.0	160	1	PETD_ORYSA	P12118 oryza sativ
41	20	100.0	163	1	PETD_SLICE	P11177 silene elae
42	20	100.0	160	1	PETD_TOBAC	P06249 nicotiana gl
43	20	100.0	160	1	PETD_WHPAT	P12119 tritium ae
44	20	100.0	160	1	UI95_HUMAN	Q9B5V1 homo sapien
45	20	100.0	160	1	UI95_MOUSE	Q9B5V2 mus musculu
46	20	100.0	161	1	PETS_CVACA	Q9B129 cyathium c
47	20	100.0	167	1	ILVH_MYCTU	Q54444 mycobacteri
48	20	100.0	168	1	ILVH_MYCTU	Q54249 mycobacteri
49	20	100.0	169	1	ILVH_MYCLE	Q33113 mycobacteri
50	20	100.0	171	1	DAPD_RUCAP	Q84590 buchnera ap

ALIGNMENTS

RESULT 1  
CD3D\_BOVIN  
ID CD3D\_BOVIN STANDARD; PPT; 59 AA.  
AC Q28072;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE T-cell surface glycoprotein CD3 delta chain precursor (T cell receptor  
DE T3 delta chain) (Fragment).  
GN CD3D.  
OS Bos taurus (Bovine).  
CC P. Karyita, Wataraka, Choudhry, Granata, Veretkova, F. K. Kostomarov;  
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
CC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-90269333; PubMed=1971793;  
RA Clevers H., Machugh R.D., Bensaïd A., Dunlap S., Baldwin C.L.,  
RA Kaushal A., Iams K., Howard C.J., Morrison W.L.;  
PT "Identification of a bovine surface antigen uniquely expressed on  
RT CD4-CD8-T cell receptor gamma/delta+ T lymphocytes.";  
PI Eur J Immunol 20:804-817(1990).  
CC -!- FUNCTION: THE CD3 COMPLEX MEDIATES SIGNAL TRANSDUCTION.  
CC -!- SUBUNIT: THE TCR/CD3 COMPLEX OF T LYMPHOCYTES CONSISTS OF EITHER  
CC A TCR ALPHA/BETA OR TCR GAMMA/DELTA HETERODIMER EXPRESSED AT THE  
CC CELL SURFACE WITH THE INVARIANT SUBUNITS OF CD3 EXPRESSED AT THE  
CC DELTA, EPSILON, ZETA, AND ETA.  
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
CC  
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CC or send an email to [license@ebi.scrib.ch](mailto:license@ebi.scrib.ch)).

EMBL: X53269; CAA37367.1;  
Immunoglobulin domain; T cell; Receptor; Transmembrane; Glycoprotein;  
Signal.  
KW SIGNAL 1 21 BY SIMILARITY.  
FT CHAIN 22 59 T CELL SURFACE GLYCOPROTEIN CD3 DELTA  
FT CHAIN 22 59 CHAIN  
FT DOMAIN 22 59 EXTRACELLULAR (POTENTIAL).  
FT CARBOHYD 38 48 N LINKED GLUCNA (POTENTIAL).  
FT NON TER 59 59  
SQ SEQUENCE 59 AA; 6468 MW; DE0C0A0A09A540E CPO04;  
Query Match 100% Score 20, TP 1; Length 59;

Best Local Similarity 100.0%, Pred No. 62,  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

QY 1 VLEP 4  
|||||  
DB 20 VLEP 20

RESULT 2  
RL32 BRUME  
ID FL32 BRUME STANDARD: PPT, 59 AA  
AC Q8YJ14;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE 50S ribosomal protein L32.  
GN RPFM OR BME10272.  
OS Brucella melitensis.  
OC Bacteria; Proteobacteria, alpha subdivision, Rhizobiaceae group,  
OC Brucellaceae; Brucella.  
OX NCBI\_TaxID=29459;  
RN [1]  
RP SEQUENCE FROM N A  
RX STRAIN=16M / ATCC 23456 / Biotype 1;  
RY MEDLINE=20020109; PubMed=11756589;  
RA DelVecchio V.G., Kapural V., Pedkar P.J., Parra G., Mujer C., Los T,  
RA Ivarova M., Anderson L., Bhattacharyya A., Lykidis A., Reznik G.,  
RA Tablonski L., Larson N., D'Souza M., Bernal A., Mazur M., Golestan E.,  
RA Selkov E., Elser F.H., Hagius S., O'Callaghan D., Leeson J.J.,  
RA Haselkorn R., Kyriides N., Overbeek R;  
RT "The genome sequence of the facultative intracellular pathogen  
RT Brucella melitensis.";  
EL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002)  
CC - SIMILARITY: BELONGS TO THE L32P FAMILY OF RIBOSOMAL PROTEINS  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))  
CC  
CC EMBL; AB009470; AAL51454.1;  
DR InterPro; IPR002677; Ribosomal L32P.  
DE Pfam; PF01793; Ribosomal L32p; 1.  
DR TIGRFAMs; TIGR01031; rplP; bact; 1.  
KW Ribosomal Protein; Compila; Proteome  
SQ SEQUENCE 59 AA, 6750 MW, 831229777075528 CPO64;  
  
Query Match 100.0%; Score 20; DB 1, Length 59,  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0,  
  
QY 1 VLEP 4  
|||||  
DB 54 VLEP 57

RESULT 3  
IF1\_LFPIIN  
ID IF1\_LFPIIN STANDARD: PPT, 71 AA.  
AC Q9XJ14;  
DT 30-MAY-2000 (Rel. 30, Created)  
DT 30-MAY-2000 (Rel. 29, Last sequence update)  
DT 15-OCT-2001 (Rel. 40, Last annotation update)  
DE Translation initiation factor IF-1.  
GN INF1.  
OS Leptospira interrogans.  
OC Bacteria; Spirochaetales; Leptospiraceae; Leptospira.  
OX NCBI\_TaxID=173,  
RN [1]  
RP SEQUENCE FROM N.A.

STRAIN=Setovar Lai;  
MEDLINE=20008945; PubMed=10620683;  
Zuener R.L., Hartkeerl R.A., van de Kemp H., Bal A.E.;  
RT "Characterization of the Leptospira interrogans S10-spc-alpha  
RT operon.";  
PL FEWS Microbiol Lett. 182:303-308(2000)  
CC - FUNCTION: NO SPECIFIC FUNCTION HAS SO FAR BEEN ATTRIBUTED TO THIS  
CC INITIATION FACTOR. HOWEVER, IT SEEMS TO STIMULATE MORE OR LESS ALL  
CC THE ACTIVITIES OF THE OTHER TWO INITIATION FACTORS, IF-2 AND IF-3.  
CC - SUBCELLULAR LOCATION: Cytoplasmic  
CC - SIMILARITY: BELONGS TO THE IF-1 FAMILY.  
CC - SIMILARITY: CONTAINS 1 SI-LIKE DOMAIN.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))  
CC  
CC EMBL; AF115283; AAD40605.1;  
DR HSP; P02998; IAH9.  
DR InterPro; IPR003029; SI.  
DE InterPro; IPR004368; TIF-IF1.  
DR Pfam; PF00575; SI; 1.  
DR SMART; SM00314; SI; 1.  
DR TIGRFAMs; TIGR00008; InfA; 1.  
DR PROSITE; PS00832; SI-IF1-TYPE; 1  
KW Initiation factor; Protein biosynthesis.  
FT INIT MET 0 0 BY SIMILARITY.  
FT DOMAIN 1 71 SI-LIKE.  
SQ SEQUENCE 71 AA, 8062 MW, 97856481214009 CPO64;  
  
Query Match 100.0%; Score 20; DB 1, Length 71;  
Best Local Similarity 100.0%; Pred. No. 77; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;  
  
QY 1 VLEP 4  
|||||  
DB 12 VLEP 15

RESULT 4  
PPIC\_ECOLI  
ID PPIC\_ECOLI STANDARD: PPT, 92 AA.  
AC P39159;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Peptidyl prolyl cis-trans isomerase C (EC 5.2.1.9) (PPIase C)  
DE (Potamase C) (Parvulin).  
GN PPIC OF EAPVA CP P377 CP 7559 CP ECS4709.  
OS Escherichia coli, and  
OS Escherichia coli O157:H7.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562, 83334;  
RN [1]  
RP SEQUENCE FROM N.A. AND SEQUENCE.  
RX MEDLINE=95010704; PubMed=7925971;  
RA Rahfeld J.-U., Ruecknagel K.P., Schelbert B., Ludwig B., Hacker J.,  
RA Mann K., Fischer G;  
PT "Confirmation of the existence of a third family among  
PT peptidyl-prolyl cis/trans isomerases. Amino acid sequence and  
PT recombinant production of parvulin.";  
RL FEBS Lett. 352:180-184(1994).  
RN [2]  
RP PRELIMINARY SEQUENCE FROM N.A  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=92358234; PubMed=1379743;  
RA Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;  
RT "Analysis of the Escherichia coli genome. DNA sequence of the region

RT from 04.5 to 06.5 minutes." ;  
 RL Science 257:771-778(1992).  
 RN [3]  
 RP REVISIONS, AND IDENTIFICATION.  
 RX MEDLINE=95184297; PubMed=7878732;  
 RA Pudd K E , Sofia H J , Koonin F V , Plunkett G. III, Lazar S.,  
 RA Rouviere P.E.;  
 RT "Conserved sequence motifs in bacterial and bacteriophage  
 RT chaperonins." ;  
 RL Trends Biochem Sci 20:14-15(1995)  
 RN [4]  
 RP SEQUENCE FROM N A  
 RC STRAIN=0157:H7 / FPL33 / ATCC 700927;  
 RX MEDLINE=21074935; PubMed=11206551;  
 RA Ferra N.T., Plunkett G. III, Rutland V., Mau P., Glasner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
 RA Posfai G., Hackett J., Klink S., Rubin A., Shao Y., Miller L.,  
 RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Peramowski F.,  
 RA Apudaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
 RA Welch R.A., Blattner F.R.,  
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";  
 RL Nature 409:629-633(2001)  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=0157:H7 / FIMO accession;  
 RX MEDLINE=21156231; PubMed=11258796;  
 RA Hayashi T., Makino Y., Ohnishi M., Kurokawa Y., Ishii K., Yokoyama K.,  
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
 RA Iida T., Takami H., Honda T., Sakakawa C., Ogisawara N., Yasunaga T.,  
 RA Kohara S., Shiba T., Hattori M., Shinagawa H.;  
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli  
 RT O157:H7 and genomic comparison with a laboratory strain K12";  
 RL DNA Res 8:11-20(2001)  
 RN [6]  
 RP SEQUENCE OF 1-21, AND CHARACTERIZATION.  
 RX MEDLINE=94215709; PubMed=8163020;  
 RA Ratfeld J.-H., Schierhorn A., Mann K., Fischer G.;  
 RT "A novel peptidyl-prolyl cis-trans isomerase from Escherichia coli";  
 RL FEBS Lett. 343:65-69(1994)  
 CC -1- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASE. IT PREFERES  
 CC AMINO ACID RESIDUES WITH HYDROPHOBIC SIDE CHAINS LIKE LEUCINE AND  
 CC PHENYLALANINE IN THE P1 POSITION OF THE PEPTIDE SUBSTRATE.  
 CC -2- CATALYTIC ACTIVITY: Peptidylproline (omega-180) = peptidylproline  
 CC (omega-0)  
 CC -3- SUBCELLULAR LOCATION: Cytoplasmic  
 CC -4- SIMILARITY: BELONGS TO THE PPI2/PAPVULIN FAMILY OF POTAMASES.  
 CC  
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 CC  
 CC EMBL: S71874, AAR2054.1;  
 CC EMBL: M87049; AAC67578.1;  
 CC EMBL: AE000454; AAC76780.1;  
 CC EMBL: AF005609; AAG58970.1;  
 CC EMBL: AF002566; BAB38132.1;  
 CC PIR: S45525; S45525.  
 CC HSP: Q13526; IPIN.  
 CC EcoGene: EG12152; ppiC.  
 CC InterPro: IPR000297; Potamase  
 CC Pfam: PF00639; Potamase; 1  
 CC PROSITE: PS01096; PPI2/PPIASE 1; 1  
 CC PROSITE: PS01098; PPI2/PPIASE 2; 1  
 KW Isomerase; Potamase; Complete Potamase  
 FT INIT\_MET 0 0  
 SQ SEQUENCE 92 AA. 101; MW. 81487.00; pI 4.70; Length 92.  
 Query March 100.00; Score 20. DR 1. Length 92.  
 Best local Similarity 100.00; Prod. No. 1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLEP 4  
 DB 70 VLEP 73  
 ID PPI2\_SALTY STANDARD; PPT; 92 AA  
 AC Q9L6S3;  
 RT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Peptidyl-prolyl cis-trans isomerase C (EC 5.2.1.8) (PPIase C)  
 DE (Potamase C) (Parvulin).  
 GN PPI2\_C ST10100 STWPI an OR STY4647.  
 OS Salmonella typhimurium, and  
 OS Salmonella typhi.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Salmonella.  
 OX NCBI\_TaxID=602, 601;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES: S. typhimurium; STRAIN: LT2 / S550412 / ATCC 14028;  
 RX MEDLINE=21534948; PubMed=11677609;  
 RA McLelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Griest M., McInerney E.,  
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Khan M.,  
 RA Waterston P., Wilson P.K.;  
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium  
 RT LT2";  
 RL Nature 413:852-856(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S typhi; STRAIN=CTL8;  
 RX MEDLINE=21534947; PubMed=11677608;  
 RA Parkhill J., Dougan G., James K.D., Thomson N.P., Pickard D., Wain J.,  
 RA Churcher C., Mungall K.L., Bentley S.P., Holden M.T.G., Sebahia M.,  
 RA Parker S., Basham D., Brooks K., Chillingworth T., Connor R.,  
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
 RA Paulwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jorgensen K.,  
 RA Krogan A., Larsen T.S., Leather S., Mello C., Moide S., Ogata P., Parry C.,  
 RA Quail M., Rutherford K., Simmonds M., Skellern J., Stevens K.,  
 RA Whitehead S., Barrall B.G.;  
 RT "Complete genome sequence of a multiple drug resistant Salmonella  
 RT enterica serovar Typhi CTL8";  
 RL Nature 413:848-852(2001).  
 CC -1- FUNCTION: PEPTIDYL-PROLYL CIS-TRANS ISOMERASE. IT PREFERES  
 CC AMINO ACID RESIDUES WITH HYDROPHOBIC SIDE CHAINS LIKE LEUCINE AND  
 CC PHENYLALANINE IN THE P1 POSITION OF THE PEPTIDE SUBSTRATE (py  
 CC similarity)  
 CC -2- CATALYTIC ACTIVITY: peptidylproline (omega-180) = peptidylproline  
 CC (omega-0).  
 CC -3- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -4- SIMILARITY: BELONGS TO THE PPI2/PAPVULIN FAMILY OF POTAMASES.  
 CC  
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 CC  
 CC EMBL: AF333324; AAF33475.1;  
 CC EMBL: AE008882; AAC22760.1;  
 CC EMBL: AL627279; CAD09407.1;  
 CC HSP: Q13526; IPIN.  
 CC StyGene: SG22222; ppiC.  
 CC InterPro: IPR000297; Potamase.  
 CC Pfam: PF00639; Potamase; 1.





Best Local Similarity 100.0%, Prod. No. 1.2e+02;  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VLEP 4  
|  
|  
|  
DB 91 VLEP 24

## RESULT 11

PEPD\_HORVU  
ID PEPD\_HORVU STANAPRO; PRT; 104 AA  
AC F12361;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Cytochrome B6-F complex subunit 4 (17 kDa polypeptide) (Fragment).  
GN PEPD.  
OS Hordeum vulgare (Barley).  
OC Chloroplast.  
CC Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,  
CC Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Poaceae,  
CC Triticeae, Hordeum.  
CX NCBI\_TaxID=4853,  
RN [1]  
PP SEQUENCE FROM N.A.  
RC STRAIN=V. Sakariis,  
RX YEASTINE 82540347, PubMed 2654887.  
RA Andreeva A.V., Buryakova A.A., Peverdatto S.V., Chakmakhecheva O.G.,  
RA Binkov V.A.;  
FT Nucleotide sequence of the 5.0 kbp barley chloroplast DNA fragment,  
FT containing psbA-psbH-pepD gene cluster.;  
RL Nucleic Acids Res. 17:2859-2860 (1989).  
CC This fragment is part of the 5.0 kbp barley chloroplast DNA fragment.  
CC COMMENTS OF THE CYTOCHROME B6-F COMPLEX  
CC 1. SUBUNIT THE MAIN SUBUNIT OF COMPLEX B6-F ARE CYTOCHROME B6,  
CC IF AKA PEPD (PEPD), CYTOCHROME F AND THE PEPD (PEPD).  
CC 2. ALTERNATIVE PRODUCTS: TWO FORMS OF THIS PROTEIN ARE PRODUCED  
CC BY ALTERNATIVE SPLICING.  
CC 3. SIMILARITY: BELONGS TO THE CYTOCHROME B6-F FAMILY, CORRESPONDS TO THE  
CC CARBOXYL END OF MITOCHONDRIAL CYTOCHROME B.  
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EMBL: X14107; CAA12269.1;  
EMBL: X14107; CAA12269.1;  
PIR: S04150; S04150.  
PIR: S09187; S09187.  
InterPro: IPR000179; Cyt b6.  
DR Pfam: PF00032; cytochrome\_b6\_c1.  
DR TIGRfam: TIGR01156; cytb6/f1v; 1.  
DR PROSITE: PS00193; CYTOCHROME B6\_Q; 1.  
KW Electron transport; Chloroplast; Photosynthesis; Transmembrane;  
KW Alternative splicing.  
FT VAPSPPLIC 1 17 MGSFSGMILKSSPIPI > MVV (IN SHOPT  
FT NON\_TER 126 136 ISOFORM)  
FT NON\_TER 126 136  
SQ SEQUENCE 104 AA; 116/1 MW; 14644AE40470F4D CIPK4;  
Query Match 100.0%, Score 20, DB 1, Length 104,  
Best local similarity 100.0%, Prod. No. 1.2e+02,  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VLEP 4  
|  
|  
|  
DB 70 VLEP 72

## RESULT 12

YF07\_ARCFU  
ID YF07\_ARCFU STANDARD; PRT; 112 AA.  
AC O28765;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein AF1507.  
GN AF1507.  
OS Archaeoglobus fulgidus.  
OC Archaea, Euryarchaeota, Archaeoglobi, Archaeoglobales;  
OC Archaeoglobaceae, Archaeoglobus  
CX NCBI\_TaxID=2234;  
RN [1]  
PP SEQUENCE FROM N.A.  
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;  
RX MEDLINE=98049343; PubMed=9389475;  
PA Flenk H-P, Clayton P.A., Tomb J-F, White O, Nelson K.E.,  
PA Richardson K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,  
PA Richardson D., Verlayage A.F., Graham D.E., Kyriades N.C.,  
PA Fleischmann P.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,  
PA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,  
PA Peterson S., Paich C.I., McNeil L.V., Badger J.H., Glodek A., Zhou L.,  
PA Overbeek P., Gocayne J.D., Weidman J.P., McDonald L., Huerbach T.,  
PA Cotton M.D., Spriggs T., Artach P., Kaine P.P., Sykes S.M.,  
PA Sadow P.W., D'Andrea Y.P., Bowman C., Fujii C., Garland S.A.,  
PA Mason T.M., Olsen G.J., Fraser C.M., Smith R.O., Woese C.R.,  
PA Venter J.C.;  
FT The complete genome sequence of the hyperthermophilic, sulphate-  
FT reducing archaeon Archaeoglobus fulgidus.;  
RL Nature 390:364-370 (1997).

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EMBL: AF000999; AAB89743.1;  
TIGR: AF1507;  
KW Hypothetical protein; Complete proteome  
SQ SEQUENCE 112 AA; 13069 MW; 6C920E43E141B42B CRC64;

Query Match 100.0%, Score 20, DB 1, Length 112,  
Best local similarity 100.0%, Prod. No. 1.3e+02,  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VLEP 4  
|  
|  
|  
DB 82 VLEP 85

## RESULT 13

RLA2\_EIMTE  
ID RLA2\_EIMTE STANDARD; PRT; 114 AA.  
AC Q967Y9;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE 60S acidic ribosomal protein P2.  
OS Eimeria tenella  
OC Eukaryota, Alveolata, Apicomplexa, Coccidia, Eimeriida, Eimeriidae;  
OC Eimeria.  
CX NCBI\_TaxID=5902,  
RN [1]  
PP SEQUENCE FROM N.A.  
RC STRAIN=PAP38;  
RA Labbe M., Pery P.;  
FT "Molecular cloning of a cDNA encoding an acidic ribosomal protein P2  
RT of Eimeria tenella.";  
PL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

```

CC -- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE ELONGATION STEP OF
CC PROTEIN SYNTHESIS (BY SIMILARITY).
CC -- SUBUNIT: P1 AND P2 EXIST AS DIMERS AT THE LARGE RIBOSOMAL
CC SUBUNIT (BY SIMILARITY).
CC -- PM- PHOSPHORYLATED (BY SIMILARITY).
CC -- SIMILARITY: RELATES TO THE VLEP FAMILY OF RIBOSOMAL PROTEINS
CC
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CC
CC EMBL: AF353514; AAK38885.1; ALT_INIT.
CC InterPro: IPR001813; 60s_ribosomal.
CC Pfam: PF00428; 60s_ribosomal; 1.
CC Ribosomal Protein: Phosphorylation.
CC SEQUENCE 114 AA; 11444 MW; 420903569078AA9 CRC64;
CC
CC Query Match 100.0%; Score 20; DB 1; Length 114;
CC Best Local Similarity 100.0%; Pred. No. 1.3e+02;
CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 VLEP 4
CC DB 26 VLEP 29
CC
CC RESULT 14
CC MERT ACICA STANDARD; PRT; 116 AA
CC ID MERT ACICA STANDARD; PRT; 116 AA
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Mercutic transport protein (Mercury ion transport protein).
CC GN MERT.
CC OS Acinetobacter calcoaceticus.
CC OG Plasmid pKLH2.
CC OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae.
CC OC Acinetobacter.
CC OX NCBI_TaxID=471;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC PX MEDLINE-94134837; PubMed 8302940.
CC RA Khodchii G.Y., Iomovskaya O.L., Gorlenko Z.M., Mindlin S.Z.,
CC Yurieva O.V., Nikiforov V.G.;
CC RT "Molecular characterization of an aberrant mercury resistance
CC transposable element from an environmental Acinetobacter strain.";
CC RL Plasmid 30:303-308(1993).
CC -- FUNCTION: INVOLVED IN MERCURIC TRANSPORT. PASSES A HG(2+) ION
CC FROM THE PERIPLASMIC MERTP PROTEIN TO THE MERCURIC REDUCTASE
CC (MERT).
CC -- SURCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (By similarity).
CC
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CC
CC EMBL: AF213017; AAA19679.1;
CC InterPro: IPR003457; Transprt_Mert.
CC Pfam: PF02411; MERT; 1.
CC KW Transport; Mercuric resistance; Inner membrane; Mercury; Plasmid;
CC Transmembrane.
CC FT TRANSMEM 16 36 POTENTIAL.
CC FT METAL 46 66
CC
CC QY 1 VLEP 4
CC DB 46 VLEP 49
CC

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FT TRANSMEM 94 114 POTENTIAL.
FT METAL 24 24 HG(2+) (BY SIMILARITY).
FT METAL 25 25 HG(2+) (BY SIMILARITY).
FT METAL 76 76 HG(2+) (BY SIMILARITY).
FT METAL 82 82 HG(2+) (BY SIMILARITY).
SQ SEQUENCE 116 AA; 12509 MW; 290903569078AA9 CRC64;
CC
CC Query Match 100.0%; Score 20; DB 1; Length 116;
CC Best Local Similarity 100.0%; Pred. No. 1.3e+02;
CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 VLEP 4
CC DB 46 VLEP 49
CC
CC RESULT 15
CC MERT ALCSP STANDARD; PRT; 116 AA
CC ID MERT ALCSP STANDARD; PRT; 116 AA
CC AC P94185;
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 15-JUN-1999 (Rel. 38, Last annotation update)
CC DE Mercutic transport protein (Mercury ion transport protein).
CC GN MERT.
CC OS Alcaligenes sp.
CC OG Plasmid IncH12 pMER610.
CC OC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
CC OC Alcaligenes.
CC OX NCBI_TaxID=512;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC PA Nikiforov V., Yurieva O., Khodchii G., Moraxella S., Gorlenko Z.,
CC Kalyaeva E., Mindlin S.;
CC RL Submitted (ECC-1996) to the EMBL/GenBank/DBJ databases.
CC -- FUNCTION: INVOLVED IN MERCURIC TRANSPORT. PASSES A HG(2+) ION
CC FROM THE PERIPLASMIC MERTP PROTEIN TO THE MERCURIC REDUCTASE
CC (MERT).
CC -- SURCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (By similarity).
CC
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CC
CC EMBL: Y08993; CAA70196.1;
CC InterPro: IPR003457; Transprt_Mert.
CC Pfam: PF02411; MERT; 1.
CC KW Transport; Mercuric resistance; Inner membrane; Mercury; Plasmid;
CC Transmembrane.
CC FT TRANSMEM 16 36 POTENTIAL.
CC FT TRANSMEM 46 66 POTENTIAL.
CC FT METAL 94 114 HG(2+) (BY SIMILARITY).
CC FT METAL 24 24 HG(2+) (BY SIMILARITY).
CC FT METAL 25 25 HG(2+) (BY SIMILARITY).
CC FT METAL 76 76 HG(2+) (BY SIMILARITY).
CC FT METAL 82 82 HG(2+) (BY SIMILARITY).
SQ SEQUENCE 116 AA; 12509 MW; AAE13C36234BAC33 CRC64;
CC
CC Query Match 100.0%; Score 20; DB 1; Length 116;
CC Best Local Similarity 100.0%; Pred. No. 1.3e+02;
CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 VLEP 4
CC DB 46 VLEP 49
CC
CC RESULT 16

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MERT_PSEAE
ID MERT_PSEAE STANDARD; PRT; 116 AA
AC P04140;
DT 01-NOV-1995 (Rel. 03, Created)
DT 01-NOV-1996 (Rel. 03, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Mercuroic transport protein (Mercury ion transport protein).
GN MERT.
OS Pseudomonas aeruginosa.
OG Plasmid pVSI
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae.
CC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC TRANSPOSOME-T501.
RA MEDLINE=85014891; PubMed=6091128;
RA Mista T.K., Brown N.L., Fritzinger D.C., Pridmore P.D., Barnes W.M.,
RA Haberstroh L., Silver S.;
RT "Mercuric ion-resistance operons of plasmid P100 and transposon
RT Tn501: the beginning of the operon including the regulatory region
RT and the first two structural genes.";
EL Proc. Natl. Acad. Sci. U.S.A. 81:1995-1997(1984).
CC - FUNCTION: INVOLVED IN MERCURIC TRANSPORT. PASSES A HG(2+) ION
CC FROM THE PERIPLASMIC MERT PROTEIN TO THE MERCURIC PEROXIDASE
CC (MERA).
CC - SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC
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CC
CC EMBL; X73112; CAA7321.1; -
CC InterPro; IPR003457; Transprt_Mert.
CC Pfam; PF02411; MERT; 1
CC Transmembrane.
CC TRANSMEM 16 36 POTENTIAL.
CC TRANSMEM 46 66 POTENTIAL.
CC TRANSMEM 94 114 POTENTIAL.
CC METAL 24 24 HG(2+) (BY SIMILARITY).
CC METAL 25 25 HG(2+) (BY SIMILARITY).
CC METAL 76 76 HG(2+) (BY SIMILARITY).
CC METAL 82 82 HG(2+) (BY SIMILARITY).
CC SEQUENCE 116 AA, 12497 MW; 53575233501F39 CP64;
Query Match 100.0%; Score 20; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 1,3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLEP 4
Db 46 VLEP 49
RESULT 18
MERT_SALTII
ID MERT_SALTII STANDARD; PRT; 116 AA.
AC P04336;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1997 (Rel. 04, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Mercuroic transport protein (Mercury ion transport protein).
GN MERT OR HCM1.234C.
OS Salmonella typhi, and
OS Shigella flexneri.
OG Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601, 623;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=CT19; PLASMID=pHCM1;
RX MEDLINE=21534947; PubMed=11677608;
RA Parthill J., Dougan G., James K.D., Thomson N.P., Pickard D., Wain J.,
RA Thutcher C., Mangill K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies P.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holecroft S., Jagers K.,
RA Krogh A., Larsen T.S., Leather S., Moulé S., O'Garra P., Parry C.,
RA Quail M., Rutherford J., Simmonds M., Skellern J., Stevens K.,

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PA Whitehead S., Barrell B.G.;  
 RT "Complete genome sequence of a multiple drug resistant Salmonella  
 enterica serovar Typhi CT18.";  
 RL Nature 413:848-852(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S.flexneri;  
 RX MEDLINE=85014891; PubMed=6091128;  
 RA Mista T.K., Brown N.L., Fritzing D.C., Pridmore R.D., Barnes W.M.,  
 Haberstroh L., Silver S.;  
 RA "Mercuric ion-resistance operons of plasmid p100 and transposon  
 Tn301: the beginning of the operon including the regulatory region  
 and the first two structural genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:5975-5979(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S.flexneri; PLASMID=IncFII NP1; TRANSDON=Trn21;  
 RX MEDLINE=85159407; PubMed=6530603;  
 RA Barrineau P., Gilbert P., Jackson W.J., Jones C.S., Summers A.C.,  
 RA Wisdom S.;  
 RT "The DNA sequence of the mercury resistance operon of the IncFII  
 plasmid NP1.";  
 RL J. Mol. Appl. Genet. 2:601-619(1984).  
 RN [3]  
 RP FROM THE PERIPLASMIC MERP PROTEIN TO THE MERCURIC REDUCTASE  
 (MERP).  
 CC -1- SUPRACELLULAR LOCATION: Integral membrane protein. Inner membrane.  
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 DR EMBL; AL513381; CAP00916.1;  
 DR EMBL; J01730; AA92261.1;  
 DR EMBL; K03089; AAR59075.1;  
 DR PIR; A04458; QCEPHT  
 DR InterPro: IPR003457; Transprt\_MerT.  
 DR Pfam; PF02411; MerT.1  
 KW Transport; Mercuric resistance; Inner membrane; Mercury; Plasmid,  
 Transmembrane; Transposable element; Complete proteome.  
 FT TRANSMEM 16 36 POTENTIAL.  
 FT TRANSMEM 46 66 POTENTIAL.  
 FT TRANSMEM 94 114 POTENTIAL.  
 FT METAL 24 24 HG(2+) (POTENTIAL).  
 FT METAL 25 25 HG(2+) (POTENTIAL).  
 FT METAL 76 76 HG(2+) (POTENTIAL).  
 FT METAL 82 82 HG(2+) (POTENTIAL).  
 SQ SEQUENCE 116 AA; 12521 MW; 8CF0744F4B0F6EE4 CRC64,  
 Query Match 100.0%; Score 20; DB 1; Length 116;  
 Best Local Similarity 100.0%; Pred. No. 1 to 100;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLEP 4  
 DB 46 VLEP 49  
 RESULT 19  
 ID MERT\_SERMA STANDARD; PRT; 116 AA.  
 AC P13112;  
 DT 01-JAN-1990 (rel. 13, Created)  
 DT 01-JAN-1990 (rel. 13, Last sequence update)  
 DT 01-NOV-1997 (rel. 35, Last annotation update)  
 DE Mercuric transport protein (Mercury ion transport protein)  
 GS MERT.  
 OS Serratia marcescens.  
 OG Plasmid pD01358.

CC Bacteria, Proteobacteria; gamma subdivision, Enterobacteriaceae;  
 CC Serratia.  
 OX NCBI\_TaxID=615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89327136; PubMed=2666393;  
 RA Nucifora G., Chu L., Silver S., Misra T.K.;  
 RT "Mercury operon regulation by the merP gene of the organomercurial  
 resistance system of plasmid pD01358.";  
 RL J. Bacteriol. 171:4241-4247(1989).  
 CC -1- FUNCTION: INVOLVED IN MERCURIC TRANSPORT. PASSES A HG(2+) ION  
 FROM THE PERIPLASMIC MERP PROTEIN TO THE MERCURIC REDUCTASE  
 (MERP).  
 CC -1- SUPRACELLULAR LOCATION: Integral membrane protein. Inner membrane.  
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 DR EMBL; M42240; AAA98122.1;  
 DR PIR; B33858; B33858.  
 DR InterPro: IPR003457; Transprt\_MerT.  
 DR Pfam; PF02411; MerT.1  
 KW Transport; Transposable element; Mercuric resistance; Inner membrane;  
 Mercury; Plasmid; Transmembrane.  
 FT TRANSMEM 16 36 POTENTIAL.  
 FT TRANSMEM 46 66 POTENTIAL.  
 FT TRANSMEM 94 114 POTENTIAL.  
 FT METAL 24 24 HG(2+) (POTENTIAL).  
 FT METAL 25 25 HG(2+) (POTENTIAL).  
 FT METAL 76 76 HG(2+) (POTENTIAL).  
 FT METAL 82 82 HG(2+) (POTENTIAL).  
 SQ SEQUENCE 116 AA; 13511 MW; 4BE13204E31A79E CRC64;  
 Query Match 100.0%; Score 20; DB 1; Length 116;  
 Best Local Similarity 100.0%; Pred. No. 1 to 100;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLEP 4  
 DB 46 VLEP 49  
 RESULT 20  
 ID REV\_HVICY STANDARD; PRT; 116 AA.  
 AC P20887;  
 DT 01-FEB-1991 (rel. 17, Created)  
 DT 01-FEB-1991 (rel. 17, Last sequence update)  
 DT 15-JUN-2002 (rel. 41, Last annotation update)  
 DE REV protein (Anti-repression transactivator protein) (ART/TPS).  
 GN REV.  
 OS Human immunodeficiency virus type 1 (OVI isolate) (HIV-1).  
 CC Viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11699;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90148544; PubMed=2559749;  
 RA Huet T., Dazza M.C., Brun-Vezinet F., Poellans G.F., Wain-Hobson S.;  
 RT "A highly defective HIV 1 strain isolated from a healthy Gabonese  
 individual presenting an atypical western blot.";  
 RL AIDS 3:707-715(1989).  
 CC -1- FUNCTION: REV APPEARS TO ACT POST TRANSCRIPTIONALLY TO RELIEVE  
 NEGATIVE REPRESSION OF gag AND env PRODUCTION.  
 CC -1- SUPRACELLULAR LOCATION: Nuclear, accumulates in the nucleoli.  
 CC -1- PPM: PHOSPHOPROTEIN WHOSE STATE OF PHOSPHORYLATION IS MEDIATED  
 BY A SPECIFIC SERINE KINASE ACTIVITY PRESENT IN THE NUCLEUS.  
 CC -1- MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A  
 HEALTHY GABONESE INDIVIDUAL.

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DR EMRL; M26727; AAA83366 1; -  
DR HIV; M26727; REV2CY1;  
DR InterPro; IPR000625; REV\_protein.  
DR Pfam; PF00424; REV; 1.  
KW Transcription regulation; AIDS; Phosphorylation; Nuclear protein.  
SQ SEQUENCE 112 AA, 1309 MW, 30650c235e4775c P0694

Query Match 100.0%, Score 20, DB 1, Length 116;  
Best Local Similarity 100.0%; Pred No. 1 3e+02;  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VLEP 4  
DB 109 VLEP 112

RESULT 21  
DRSD ARCFU  
ID EHS2\_APCFV STANDARD, PFT, 117 AA  
AC 029573;  
DT 16-OCT-2001 (Pel. 40, Created)  
DT 16-OCT-2001 (Pel. 40, Last sequence update)  
DT 15-JUN-2002 (Pel. 41, Last annotation update)  
DE Succinate dehydrogenase hydrophobic membrane anchor protein.  
GN SCHD OP AF0684.  
OS Archaeoglobus fulgidus  
OC Archaea, Euryarchaeota; Archaeoglobi; Archaeoglobales;  
OC Archaeoglobaceae; Archaeoglobus  
OX NCBI\_TaxID=2234,  
RN [1]\_TaxID=2234,  
PP SEQUENCE FROM N.A.  
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;  
RX MEDLINE=98049343; PubMed=9389475;  
RA Fleck H.E., Clayton P.A., Tomlin J.F., White G., Nelson F.E.,  
PA Ketchum K.A., Dodson P.J., Gwin M., Hickey E.K., Peterson J.D.,  
PA Richardson D.L., Kesteven A.P., Graham D.E., Kyrtides N.C.,  
PA Plickmann P.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,  
PA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,  
RA Peterson S., Reich C.L., McNeil L.K., Badger J.H., Glodex A., Zhou L.,  
RA Svetlizek F., Gwynne C.D., Weidman J.F., MacDonald L., Unterbach T.,  
RA Cotton M.D., Spriggs T., Artach P., Kane B.P., Sykes S.M.,  
RA Sadov P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,  
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,  
RA Venter J.C.;  
RT "The complete genome sequence of the hyperthermophilic, sulphate-  
RT reducing archaeon Archaeoglobus fulgidus.",  
RL Nature 390:364-370(1997).

CC 1- FUNCTION: PUTATIVE HYDROPHOBIC COMPONENT OF THE SUCCINATE  
CC FERRHYDROGENASE COMPLEX. COULD BE REQUIRED TO ANCHOR THE CATALYTIC  
CC COMPONENTS TO THE CYTOPLASMIC MEMBRANE (BY SIMILARITY).  
CC 1- PATHWAY: Tricarboxylic acid cycle.  
CC 1- SUBUNIT: PART OF AN ENZYME COMPLEX CONTAINING FOUR SUBUNITS A  
CC FLAVOPROTEIN, AN IRON-SULFUR, CYTOCHROME B-556, AND AN HYDROPHOBIC  
CC ANCHOR PROTEIN (BY SIMILARITY).  
CC 1- SUBCELLULAR LOCATION: Integral membrane protein (Probable)

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DR EMRL; AE001057; AAB90554.1; -  
DR TIGR; AF0684; -  
DR InterPro; IPR000701; Sdh\_cyt.  
DR Pfam; PF01127; Sdh\_cyt; 1.  
KW Tricarboxylic acid cycle; Electron transport; Heme; Transmembrane;  
KW Complete proteome.  
FT TRANSMEM 10 30 POTENTIAL.  
FT TRANSMEM 63 83 POTENTIAL.  
FT TRANSMEM 97 117 POTENTIAL.  
FT BINDING 73 73 HEME (BY SIMILARITY).  
SQ SEQUENCE 117 AA, 13100 MW, 7289CF914F52B7D3 C0664;

Query Match 100.0%, Score 20, DB 1, Length 117;  
Best Local Similarity 100.0%; Pred No. 1 3e+02;  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VLEP 4  
DB 10 VLEP 13

RESULT 22  
SYE STAXY  
ID SYE STAXY STANDARD, FRT, 120 AA.  
AC P77984;  
DT 15-DEC-1998 (Pel. 37, Created)  
DT 15-DEC-1998 (Pel. 37, Last sequence update)  
DT 16 OCT-2001 (Pel. 40, Last annotation update)  
DE Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate-tRNA ligase)  
DE (Glut) (Fragment).  
GN GLTX.  
OS Staphylococcus xylosus.  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
OX NCBI\_TaxID=1288;  
RN [1]\_TaxID=1288;  
PP SEQUENCE FROM N.A.  
RC STRAIN=DSM 20267 / Isolate C5A;  
RX MEDLINE=97237691; PubMed=9084146;  
RA Fiedler H., Brueckner R.;  
RT "Identification of the serine acetyltransferase gene of Staphylococcus  
RT xylosus.",  
RL FEMS Microbiol. Lett. 149:181-187(1997).  
CC 1- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +  
CC diphosphate + L-glutamyl-tRNA(Glu).  
CC 1- SUBUNIT: MONOMER (BY SIMILARITY).  
CC 1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC 1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.

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DR EMRL; Y07614; CAA68866 1; -  
DR InterPro; IPR000324; Glu\_tRNA-synt\_1c  
DR Pfam; PF00749; tRNA-synt\_1c; 1.  
DR Pfam; PF00749; tRNA-synt\_1c; 1.  
DR PROSITE; PS00178; AA\_TRNA\_LIGASE\_1; PARTIAL.  
KW Aminoacyl-tRNA synthetase, Protein biosynthesis; Ligase; ATP-binding.  
FT NON\_TER 1  
SQ SEQUENCE 120 AA, 13638 MW, 6A2CE7FC1332C763 C0664;

Query Match 100.0%, Score 20, DB 1, Length 120;  
Best Local Similarity 100.0%; Pred No. 1 4e+02;  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VLEP 4  
DB 56 VLEP 59

RESULT 23  
MERT\_ENTAG  
ID MERT\_ENTAG STANDARD; PPT: 126 AA  
AC P94760;  
DT 01-NOV-1997 (Rel. 35, last sequence update)  
DT 01-NOV-1997 (Rel. 35, last sequence update)  
DT 15-JUN-2002 (Rel. 41, last annotation update)  
DE Mercuric transport protein (Mercury ion transport protein)  
GN MERT.  
OS Enterobacter agglomerans (Pantoea agglomerans).  
OG Plasmid pK1H272.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae;  
OC Pantoea.  
OX NCBI\_TaxID=549;  
RN [1]\_TaxID=549;  
RP SEQUENCE FROM N.A.; PubMed=9703088; PubMed=9159519;  
RX MEDLINE=9703088; PubMed=9159519;  
RA Yutseva O., Kholodil G., Minakhin L., Gorlenko Z., Kalyaeva E.,  
FA Mindlin S., Nikiforov V.;  
RT "Interferon-indeled spread of promiscuous mercury-resistance  
transposons in environmental bacteria";  
RL Mol. Microbiol. 24:321-329(1997)  
CC FUNCTION: INVOLVED IN MEROPHILIC TRANSPOSE PASSAGE A HG(2+) ION  
FROM THE PERIPLASMIC MEMBRANE PROTEIN TO THE MEROPHILIC PROTEINASE  
(MERP)  
CC (BY SIMILARITY)  
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CC  
DR FMR; Y08992; CAA70186.1;  
DI InterPro: IPR003457; Transp\_Mert.  
KW Pfam: PF02411; MERT; 1.  
KW Transport; Mercuric resistance; Inner membrane; Mercury; Plasmid,  
KW Transmembrane.  
FT TRANSMEM 26 46 POTENTIAL.  
FT TRANSMEM 54 74 POTENTIAL.  
FT TRANSMEM 104 124 POTENTIAL.  
FT METAL 34 34 HG(2+) (BY SIMILARITY).  
FT METAL 35 35 HG(2+) (BY SIMILARITY).  
FT METAL 86 86 HG(2+) (BY SIMILARITY).  
FT METAL 92 92 HG(2+) (BY SIMILARITY).  
SQ SEQUENCE 126 AA, 13664 MW, 20484RPF5A7D0F QP64,  
Query Match 100.0%, Score 20, DB 1, Length 126,  
Best Local Similarity 100.0%, Pred. No. 1.5e+02,  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VLEP 4  
DB 56 VLEP 59  
RESULT 24  
UMPI\_SCHPO  
ID UMPI\_SCHPO STANDARD; PPT: 129 AA.  
AC O74416;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Putative proteasome maturation factor umpl  
GN SPOC1410.03C.  
OS Schizosaccharomyces pombe (Fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.

OX NCBI\_TaxID=4896;  
RN [1]\_TaxID=4896;  
RP SEQUENCE FROM N.A.  
PC STRAIN=972;  
RX MEDLINE=21848401; PubMed=11859360,  
PA Wood V., Gwilliam P., Pajandream M.A., Lyne M., Lyne P., Stewart A.,  
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
RA Collins M., Connor P., Cronin A., Davis P., Fellwell T., Fraser A.,  
PA Gentles S., Goble A., Hamlin N., Harris D., Hildalgo J., Hudson G.,  
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt C., Jorgensen K.,  
RA Jones K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
PA Money K., Moule S., Mungall F., Murphy L., Niblett D., Odell C.,  
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitz E.,  
RA Rutherford K., Putter S., Saunders D., Seeger K., Sharp S.,  
PA Skelton J., Simmonds M., Squares R., Stevens S., Warren T., Whitehead S.,  
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
PA Woodward J., Volckaert G., Aert P., Robben J., Grympeprez B.,  
RA Welljens I., Vanstreels E., Pieger M., Schaefer M., Mueller-Auer S.,  
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl P., Hilbert H.,  
PA Beyer K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,  
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,  
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,  
PA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thore G.,  
PA Daga P., Cruzado I., Gimenez J., Sanchez M., del Roy P., Perito L.,  
PA Geringuer A., Revuelta J.L., Marenc J., Armering J., Feschel S.L.,  
RA Cerutti L., Lowe T., McCombie W.F., Paulsen I., Potashkin J.,  
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;  
RT "The genome sequence of Schizosaccharomyces pombe";  
PL Nature 415:871-880(2002).  
CC FUNCTION: SHORT-LIVED TRAFFICOR PRESENT IN THE PERIPLASMIC FORM OF  
THE TCS PROTEASOME AND ABSENT IN THE MATURE COMPLEX. REQUIRED FOR  
THE CORRECT ASSEMBLY AND ENZYMIC ACTIVATION OF THE PROTEASOME  
(BY SIMILARITY).  
CC  
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CC  
EMBL: AL031518; CAA20656.1;  
KW Hypothetical protein; Proteasome; Chapterone.  
DR Hypothetical protein; Proteasome; Chapterone.  
SQ SEQUENCE 129 AA, 14661 MW, 360AE66B33BE4C1 QP664;  
Query Match 100.0%, Score 20, DB 1, Length 129,  
Best Local Similarity 100.0%, Pred. No. 1.5e+02,  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VLEP 4  
DB 21 VLEP 24  
RESULT 25  
YIOL\_YEAST  
ID YIOL\_YEAST STANDARD; PPT: 129 AA.  
AC P40461;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Hypothetical 14.4 kDa protein in OCT2-AX12 intergenic region.  
GN YIOL141W.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycetina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]\_TaxID=4932;  
RP SEQUENCE FROM N.A.  
PC STRAIN=S288C / AB972;

RA Barrett B.G., Badcock K., Rankier A.T., Bowman S., Brown D.,  
 RA Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,  
 RA Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,  
 RA Louis F., Lye G., Moule S., Moule T., Odell C., Pearson D.,  
 RA Pajandream M.A., Piles L., Powley N., Skelton J., Smith V.,  
 RA Walsh S.V., Whitehead S.;  
 PL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases  
 CC -----  
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 CC -----  
 DR EMBL; Z38059; CAA86137.1; -.  
 DR PIR; S48393; S48393.  
 DP SGD; S0001403; YII141W.  
 KW Hypothetical protein.  
 SQ SEQUENCE 125 AA; 14437 MW; 4A1891980F5BF77R CEC64;  
  
 Query Match 100.0%; Score 20; DB 1; Length 129;  
 Best Local Similarity 100.0%; Pred. No. 1.Se+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 VLEP 4  
 DB 7 VLEP 10

Search completed: March 5, 2003, 09:32:46  
 Job time : 31 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: March 5, 2003, 04:40:05 : Search time 24 seconds  
(without alignments)  
24 423 Million cell updates/sec

Title: US-09-732-411-15  
Percent score: 20  
Sequence: 1 VLEP 4

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 6

Maximum DB seq length: 200000000

Post-processing: Minimum Match 98%

Maximum Match 100%

Listing first 50 summaries

Database: sptpwmr1\_21.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rv.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	25	Q9RM55	Q9RM55 chione carc
2	20	100.0	26	Q9RM52	Q9RM52 moniliform
3	20	100.0	30	Q9WJ19	Q9WJ19 gallus gall
4	20	100.0	43	Q9WJ16	Q9WJ16 canine dist
5	20	100.0	47	Q9SP47	Q9SP47 spartina an
6	20	100.0	47	Q9SP46	Q9SP46 spartina ma
7	20	100.0	47	Q9SP45	Q9SP45 pseudomonas
8	20	100.0	52	Q9PWW3	Q9PWW3 homo sapien
9	20	100.0	55	Q96P44	Q96P44 calicivirus
10	20	100.0	58	Q9AC31	Q9AC31 calicivirus
11	20	100.0	64	Q9AC32	Q9AC32 chilo iride
12	20	100.0	61	Q95728	Q95728 sulfolobus
13	20	100.0	62	Q97US6	Q97US6 hordeum vul
14	20	100.0	63	Q96EX8	Q96EX8 staphylococ
15	20	100.0	63	Q99WL3	Q99WL3 methylobact
16	20	100.0	64	Q96120	

17	20	100.0	65	3	Q14380	Q14380 schizosacch
18	20	100.0	68	16	Q9QCV7	Q9QCV7 arab thieric
19	20	100.0	71	13	Q9QWY7	Q9QWY7 cestuvis co
20	20	100.0	74	11	Q9QJ82	Q9QJ82 mus musculu
21	20	100.0	77	16	Q9QW60	Q9QW60 streptomyces
22	20	100.0	77	17	Q9VE13	Q9VE13 streptomyces
23	20	100.0	79	11	Q97585	Q97585 ratia novy
24	20	100.0	80	5	Q91470	Q91470 caenorhabdi
25	20	100.0	81	12	Q9QCV6	Q9QCV6 canipe dist
26	20	100.0	81	17	Q9QXSC	Q9QXSC calicivirus
27	20	100.0	82	8	Q93399	Q93399 zea mays lm
28	20	100.0	82	12	Q99530	Q99530 human hepe
29	20	100.0	83	5	Q18436	Q18436 caenorhabdi
30	20	100.0	83	16	Q9WVDS	Q9WVDS streptomyces
31	20	100.0	84	12	Q9VAC4	Q9VAC4 beta-titina
32	20	100.0	85	9	Q9ME37	Q9ME37 baculophia
33	20	100.0	96	12	Q9VAA3	Q9VAA3 white spot
34	20	100.0	96	17	Q27827	Q27827 methanobact
35	20	100.0	98	4	Q9MX28	Q9MX28 homo sapien
36	20	100.0	99	16	Q9X076	Q9X076 theimotota
37	20	100.0	99	15	Q74888	Q74888 human immun
38	20	100.0	99	15	Q74889	Q74889 human immun
39	20	100.0	99	15	Q91CNG	Q91CNG human immun
40	20	100.0	99	15	Q91CNI	Q91CNI human immun
41	20	100.0	99	6	Q9N001	Q9N001 macaca fasc
42	20	100.0	99	2	Q56223	Q56223 theimotota
43	20	100.0	99	5	Q44041	Q44041 plasmodium
44	20	100.0	99	5	Q44042	Q44042 plasmodium
45	20	100.0	99	5	Q44043	Q44043 plasmodium
46	20	100.0	99	5	Q44044	Q44044 plasmodium
47	20	100.0	99	5	Q44046	Q44046 plasmodium
48	20	100.0	99	9	Q9AZV3	Q9AZV3 bacterioph
49	20	100.0	99	16	Q9QDQ4	Q9QDQ4 bacteriococ
50	20	100.0	99	10	Q9PS79	Q9PS79 cytt raly

## ALIGNMENTS

### RESULT 1

ID	Q9RM55	PRELIMINARY;	PRT;	25 AA.
AC	Q9RM55;			
DT	01-JUN-2001 (TREMURel 17, Created)			
DT	01-JUN-2001 (TREMURel 17, last sequence update)			
DT	01-JUN-2001 (TREMURel 17, last annotation update)			
DE	LINE-like reverse transcriptase (Fragment).			
OS	Chione cancellata.			
CC	Eukaryota; Metazoa; Mollusca; Bivalvia; Heterodonta; Veneroida;			
OC	Veneroidae; Veneridae; Chione.			
CX	NCBI_TaxID:145464.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
PC	TRANSPORIN LST-11 PETROTRANSPORIN;			
RX	MEDLINE=20570504; PubMed=11121049;			
RA	Arkhipova I., Meselson M.;			
RT	"Transposable elements in sexual and asexual taxa";			
PL	Proc. Natl. Acad. Sci. U.S.A. 97:14473-14477(2000).			
DR	EMBL: AY013938; AAC59923.1; ..			
KW	RNA-directed DNA polymerase.			
FT	NON TER 1			
FT	NON TER 25			
SQ	SEQUENCE 25 AA, 2732 MW, 113515FFC4AC2A7 CEM64;			

Query Match: 100.0%, Score 20, DP 5, Length 25;

Best local Similarity: 100.0%, Prod No. 2.2e+02;

Matches: 4; Conservativ: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 VLEP 4

Db 2 VLEP 5



DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
 DE Ribosomal protein L16 (Fragment)  
 GN RPL16.  
 OS Spartina anglica  
 OG Chloroplast.  
 OC Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,  
 OC Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade,  
 OC Chloridoideae, Cynodonteae, Spartina.  
 OX NCBI\_TaxID=49786;  
 RN [1]  
 PP SEQUENCE FROM N.A.  
 RA Baumeil A., Ainouche M.L., Levasseur J.-E.,  
 PT "Molecular investigations in populations of *Spartina anglica* C. E.  
 RT Hubbard invading coastal Brittany (France)."  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF276969; AAK71926.1;  
 DR InterPro: IPR000114; Ribosomal\_L16  
 DR Pfam: PF00252; Ribosomal\_L16, 1.  
 KW Chloroplast.  
 FT NON\_TER 1 47  
 FT NON\_TER 47 47  
 SQ SEQUENCE 47 AA; 6670 MW; 108910AA7C77721 7564;

Query Match 100.0%; Score 20; DP 8; Length 47;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4  
 DB 35 VLEP 38

RESULT 7  
 Q95F85 PRELIMINARY; PRT; 47 AA.  
 ID Q95F85  
 AC Q95F85;  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
 DE Ribosomal protein L16 (Fragment)  
 GN RPL16.  
 OS Spartina maritima.  
 OG Chloroplast.  
 OC Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,  
 OC Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade,  
 OC Chloridoideae, Cynodonteae, Spartina.  
 OX NCBI\_TaxID=49786;  
 RN [1]  
 PP SEQUENCE FROM N.A.  
 RA Baumeil A., Ainouche M.L., Levasseur J.-E.,  
 PT "Molecular investigations in populations of *Spartina anglica* C. E.  
 RT Hubbard invading coastal Brittany (France)."  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases  
 DR EMBL: AF276970; AAK71926.1;  
 DR InterPro: IPR000114; Ribosomal\_L16.  
 DR Pfam: PF00252; Ribosomal\_L16, 1.  
 KW Chloroplast.  
 FT NON\_TER 1 47  
 FT NON\_TER 47 47  
 SQ SEQUENCE 47 AA; 6674 MW; 108910AA7C77721 7564;

Query Match 100.0%; Score 20; DP 8; Length 47;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4  
 DB 35 VLEP 38

RESULT 8

Q96FW3 PRELIMINARY; PRT; 52 AA.  
 ID Q96FW3  
 AC Q96FW3;  
 DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TRENBLrel. 21, Last annotation update)  
 DE Mercutic ion transport protein (Fragment)  
 GN MEPT.  
 OS Pseudomonas putida.  
 OC Bacteria, Proteobacteria, gamma subdivision, Pseudomonadaceae;  
 OC Pseudomonas.  
 OX NCBI\_TaxID=303;  
 RN [1]  
 PP SEQUENCE FROM N.A.  
 RA STEINMETZ J., TRANSPONSON-TN5041D;  
 PA Khodadi G.Y., Michlin S.Z., Gellera C.M., Bass I.A., Poljanec P.S.,  
 RA Nikiforov V.;  
 RT "Host-dependent transposition of Tn5041."  
 RT Puss J. Genet. 32:365-373(2000).  
 DR EMBL: Y18977; CAB8562.1.  
 DR InterPro: IPR001457; Transprt\_MerT.  
 DR Pfam: PF02411; MerT, 1.  
 FT NON\_TER 52  
 FT NON\_TER 52 52  
 SQ SEQUENCE 52 AA; 5200 MW; E670E624328E412 7564;

Query Match 100.0%; Score 20; DP 2; Length 52;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4  
 DB 46 VLEP 49

RESULT 9  
 Q96FP4 PRELIMINARY; PRT; 55 AA.  
 ID Q96FP4  
 AC Q96FP4;  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE Unknown (protein for MGC:182116).  
 OS Homo sapiens (Human).  
 OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,  
 OC Mammalia, Eutheria, Primates, Catarrhini, Hominoidea, Homo.  
 OX NCBI\_TaxID=9606,  
 RN [1]  
 PP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RA Strausberg R.;  
 PL Submitted (JUL 2001) to the FMBL/GenBank/DBJ databases.  
 DR EMBL: BC010607; AAH10607.1;  
 SQ SEQUENCE 55 AA; 6011 MW; 191A77612A7967EE 7564;

Query Match 100.0%; Score 20; DP 4; Length 55;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4  
 DB 6 VLEP 9

RESULT 10  
 Q96G31 PRELIMINARY; PRT; 58 AA.  
 ID Q96G31  
 AC Q96G31;  
 DT 01-JAN-1998 (TRENBLrel. 05, Created)  
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)  
 DT 01-OCT-2001 (TRENBLrel. 18, Last annotation update)  
 DE Capsid protein (Fragment).  
 OS Calicivirus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae.

```

OX NCBI_TaxID=11975;
RN
RC SEQUENCE FROM N.A.
RC STRAIN B453/92/UK.
RX MEDLINE=97278118, PubMed=9131452,
RA Green S.M., Lambden P.R., Owen G.A., Clarke I.N.;
RT "Capsid sequence diversity in small round structured viruses from
RT recent UK outbreaks of gastroenteritis.";
RL J. Med. Virol. 52:114-19(1997).
DR EMBL: Z73927; CAAG820911;
DE InterPro: IPR004005; Calici_coat
DR Pfam: PF00915; Calici_coat; 1
FT NON_TER 1
FT NON_TER 58
SQ SEQUENCE 58 AA; 4086 MW; CA987C193R9CQ02D CRC64;

Query Match 100.0%; Score 20; DB 12; Length 58;
Best local similarity 100.0%; Pred No 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 50 VLEP 53

RESULT 11
O39632 PRELIMINARY; FET; 19 AA.
ID O39632
AC O39632; (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Capsid protein (Fragment).
OS Calicivirus
CC Viruses: ssRNA positive strand viruses, no DNA stage, Caliciviridae
CX NCBI_TaxID=11975;
RN
RC SEQUENCE FROM N.A.
RC STRAIN-CAPMAPHER/94/UK.
RX MEDLINE=97278118, PubMed=9131452;
RA Green S.M., Lambden P.R., Owen G.A., Clarke I.N.;
RT "Capsid sequence diversity in small round structured viruses from
RT recent UK outbreaks of gastroenteritis.";
RL J. Med. Virol. 52:114-19(1997)
DR EMBL: Z73927; CAAG820911;
DE InterPro: IPR004005; Calici_coat.
DR Pfam: PF00915; Calici_coat; 1.
FT NON_TER 1
FT NON_TER 58
SQ SEQUENCE 58 AA; 4087 MW; A3F42F412441D CRC64;

Query Match 100.0%; Score 20; DB 12; Length 58;
Best local similarity 100.0%; Pred No 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 50 VLEP 53

RESULT 12
O55728 PRELIMINARY; FET; 61 AA.
ID O55728
AC O55728; (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Hypothetical 7.4 kDa protein.
OS Chilo iridescent virus (CIV) (Insect iridescent virus type 6).
CC Viruses, ssRNA viruses, no RNA stage, Iridoviridae, Iridovirus.
CX NCBI_TaxID=10489;
RN
RC SEQUENCE FROM N.A.
RA Bahr U., Tidona C.A., Darai G.;
RL Virus Genes 0:0-0(1997).
DR EMBL: AF303741; AAR04439 1; -.
RW Hypothetical protein.
SQ SEQUENCE 61 AA; 7395 MW; AF71RA75RC14AE0A CRC64;

Query Match 100.0%; Score 20; DB 12; Length 61;
Best local similarity 100.0%; Pred No 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 53 VLEP 56

RESULT 13
Q97US6 PRELIMINARY; PPT; 62 AA.
ID Q97US6
AC Q97US6; (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Second OPP in transposon ISCI058.
GN SSO11456.
OS Sulfolobus solfataricus.
CC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
CX Sulfolobus.
CX MFP: T3x12-2287;
RN
RC SEQUENCE FROM N.A.
RC STRAIN-ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=97278118, PubMed=9131452;
RA Ste G., Singh P.K., Gangadhari P., Sivaprasad V., Allard G.,
PA Aways M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
PA De Meers A., Ebrause G., Fletcher C., Gordon P.W.V.,
PA Heikamp-de Jung T., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
PA Thi-Ngoc H.P., Redder P., Schenk W.F., Thariail C., Polstrup N.,
PA Charlebois P.L., Doolittle W.F., Duquet M., Gaasterland T.,
PA Carlett P.A., Fyfe M.A., Jensen G.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2."
PL PROC. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
DR EMRL: AE006881; AAK41026 1; -
RW Complete Proteome.
SQ SEQUENCE 62 AA; 6561 MW; C2BCEBPB13P43FF CRC64;

Query Match 100.0%; Score 20; DB 17; Length 62;
Best local similarity 100.0%; Pred No 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 20 VLEP 23

RESULT 14
Q9FEX8 PRELIMINARY; PPT; 63 AA.
ID Q9FEX8
AC Q9FEX8; (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE Putative lectin (Fragment).
GN HL2.
OS Hordeum vulgare (Barley).
CC Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Charophyta;
CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
CC Tricaceae; Hordeum.
CX NCBI_TaxID=4513;
RN
RC SEQUENCE FROM N.A.
RC TISSUE-ETIOLOGED COLEOPTILE;
RW Klopstech K.R.;
RA Klopstech K.R.;
RL Submitted (01-03-2000) to the EMBL/GenBank/CCRP databases.

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RN  [2]
RP  SEQUENCE FROM N.A.
RC  TISSUE=ETIOLOGICAL COLLEPTILE;
RA  Grunwald I.;
RL  Thesis (2001), Department of Biological Sciences,
PL  University of Hannover, Hannover, Germany.
DP  EMBL; AC030112; CAC19669.1; -.
KW  Lectin.
FT  NON_TER 1 63
FT  NON_TER 63 63
SQ  SEQUENCE 63 AA; 6948 MW; D794D32B1A5A8C93 CR064;

Query Match 100.0%; Score 20; PR 16; Length 63;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 54 VLEP 57

RESULT 15
Q99WL3 PRELIMINARY; PRT; 63 AA.
AC Q99WL3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein SAV0364
GN SAV0364 OP SAV0361 OP SAS009
OS Staphylococcus aureus (strain M50 / ATCC 26695), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
OX NCBI_TaxID=158878, 158879;
RN [1]_TaxID=158878, 158879;
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain M50), and S.aureus (strain N315);
RX MEDLINE=2111952, PubMed=1141814;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Ouchi A., Aoki K.-I., Nagai Y., Imai T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue P.-I., Fatio C.,
RA Sekimizu K., Hirakawa H., Fuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancet 357:1225-1243(2001)
DR EMBL; AF003359; BAB56526.1; -.
DR EMBL; AF003130; BAB41576.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 63 AA; 7061 MW; 4B06A0A5A5A5A5A5 CR064;

Query Match 100.0%; Score 20; PR 16; Length 63;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 35 VLEP 38

RESULT 16
O05120
ID O05120 PRELIMINARY; PRT; 64 AA.
AC O05120;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to a putative orf in the mgsB region of Phodabacter
DE sphaeroides (Fragment)
OS Methylobacterium extorquens.

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Methylobacterium group; Methylobacterium.
OX NCBI_TaxID=408;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AM1;
RX MEDLINE=97386438; PubMed=9244287;
RA Chistoserdova L., Lidstrom M.E.;
RT "Identification and mutation of a gene required for glyoxylate kinase
RT activity from a facultative methylotroph, Methylobacterium extorquens
RT AM1.";
RL J. Bacteriol. 179:4946-4948(1997).
RF EMBL; Y87316; AAE66500.1; -.
DR InterPro; IPR001449; TPR.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 64 AA; 7417 MW; F28A40CC4D121E7F CR064;

Query Match 100.0%; Score 20; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 6 VLEP 9

RESULT 17
O14390 PRELIMINARY; PRT; 65 AA.
ID O14390;
AC O14390;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 7.4 kDa protein (Fragment).
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX NCBI_TaxID=4896;
RN [1]_TaxID=4896;
RP SEQUENCE FROM N.A.
RC STRAIN=972H;
RA Jiang Y.-J., Yoo H.-S.;
PL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U97376; AAB63868.1; -.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 65
SQ SEQUENCE 65 AA; 7163 MW; 553E915F67E34824 CR064;

Query Match 100.0%; Score 20; DB 3; Length 65;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 29 VLEP 32

RESULT 18
Q92QK7 PRELIMINARY; PRT; 68 AA.
ID Q92QK7;
AC Q92QK7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 13, Last annotation update)
DE At2G07350 protein.
GN At2G07350.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicot; Fossidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;

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BN SEQUENCE FROM N.A.  
 PP STRAIN=CV. COLOMBIA;  
 RX MELLINE-25083497; PubMed=16617197;  
 RA Lin X., Kaul S., Pounsley S.D., Shea T.P., Benito M.-I., Town C.D.,  
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.P., Feldblum T.V.,  
 RA Puell C.P., Kechter V.A., Lee J.J., Ponnig C.M., Koo H., Moffat K.S.,  
 RA Cronin L.A., Shen M., VanAken S.E., Unayam L., Tallon L.J., Gill J.E.,  
 RA Adams W.D., Gillingham A.J., Tinsley T.H., Grogan H.M., Somerville C.R.,  
 RA Copenhagen G.P., Preuss D., Niernan W.C., White G., Eisen J.A.,  
 RA Salzberg S.L., Fraser C.M., Venter J.C.;  
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis  
 thaliana";  
 RL Nature 402:761-768 (1999).  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLOMBIA;  
 RA Lin X.,  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DP EMBL: AC004217; AAC15527.1; -  
 SQ SEQUENCE 68 AA; 7727 MW; 6A67C97FB999FDCE0 CPC64;

Query Match 100.0%; Score 20; DB 10; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 6 aa+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4  
 DB 6 VLEP 9  
 RESULT 19  
 ID Q90WY7 PRELIMINARY; PPT; 71 AA.  
 AC Q90WY7  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Agouti-related protein (fragment).  
 OS Coturnix coturnix japonica (Japanese quail)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopteria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 CC Coturnix;  
 CX NCBI\_TaxID=93934;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-HYPOTHALAMUS;  
 RA Buswell T., Li Q., Takeuchi S.;  
 RT "Neurons expressing neuropeptide Y mRNA in the infundibular  
 hypothalamus of Japanese quail are activated by fasting and co-express  
 agouti-related protein mRNA";  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY048849; AAL06600.1; -  
 FT NON-TER  
 SQ SEQUENCE 71 AA; 7866 MW; EF0412E7A71B22 CPC64;

Query Match 100.0%; Score 20; DB 13; Length 71;  
 Best Local Similarity 100.0%; Pred. No. 6 aa+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4  
 DB 3 VLEP 6  
 RESULT 20  
 ID Q9UJ82 PRELIMINARY; PPT; 74 AA.  
 AC Q9UJ82  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Brain cDNA clone MNCB-2875.

GN A030009H04PIK  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus;  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CS7BL;  
 RA Osada N., Kusuda J., Tanuma P., Ito A., Hirata M., Sugano S.,  
 RA Hashimoto K.;  
 RT "Isolation of full-length cDNA clones from mouse brain cDNA library  
 made by oligo-cuffing method";  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB041807; BAA35115.1; -  
 DP MGD: MGI:1915159; A030009H04PIK  
 SQ SEQUENCE 74 AA; 8117 MW; 606971BF026BF5E9 CPC64;

Query Match 100.0%; Score 20; DB 11; Length 74;  
 Best Local Similarity 100.0%; Pred. No. 6 aa+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4  
 DB 42 VLEP 45  
 RESULT 21  
 ID Q99Q00 PRELIMINARY; PPT; 77 AA.  
 AC Q99Q00  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Hypothetical protein SCPI.332.  
 GN SCPI 332 ANP SCPI 22c  
 OS Streptomyces coelicolor  
 OG Plasmid SCPI.  
 CC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 CC Actinomycetales; Streptomycesaceae; Streptomycesaceae; Streptomyces;  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Bentley S.D., Chater K.P., Cardeno-Tarraga A.-M., Challis G.L.,  
 RA Thomson N.P., James K.D., Harris D.E., Quail M.A., Kieser H.,  
 RA Hafter D., Pateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
 RA Huang C.H., Kiser T., Larke L., Murphy L., Oliver K., O'Neill S.,  
 RA Rabinowitch E., Rajandream M.A., Rutherford K., Sitter S.,  
 RA Seeger F., Saunders D., Sharp S., Squares P., Squares S., Taylor K.,  
 RA Warren T., Wietzorek A., Woodward J., Barrall R.G., Parkhill C.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomycete Streptomyces  
 coelicolor A3(2)";  
 RL Nature 417:141-147 (2002)  
 DP EMBL: AL590464; CAC36857.1; -  
 CP EMBL: AL590464; CAC36544.1; -  
 KW Hypothetical protein; Plasmid.  
 SQ SEQUENCE 77 AA; 8145 MW; 69E94CE9224F08 CPC64;

Query Match 100.0%; Score 20; DB 16; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 6 aa+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4  
 DB 71 VLEP 74  
 RESULT 22  
 ID Q9VEI3 PRELIMINARY; PPT; 77 AA.  
 AC Q9VEI3

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DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Hypothetical protein APE5025.
GN APE5025.
OS Aetopyrum pernix.
OC Archaea: Crenarchaeota: Thermopicrobi: Desulfurococcales;
OC Desulfurococaceae; Aetopyrum
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=98310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Hatikawa Y.,
RA Jinno K., Takahashi M., Sekine M., Baba S.-I., Ankaï A., Kosugi H.,
RA Hosoyama A., Fukui S., Naito Y., Nishitani K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudo Y.,
RA Yamazaki J., Kishida N., Omori A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aetopyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
DR EMBL: AP000060; HAA70563.1; -
PW Hypothetical protein, complete protein
SQ SEQUENCE // AA: 4700 MW; 4261c9d8e41f552a cpc64;

Query Match 100.0%; Score 20; DB 17; Length 77;
Best Local Similarity 100.0%; Pred. No. 6 Re+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 10 VLEP 33

RESULT 23
P97585
ID P97585 PRELIMINARY; PPT; 79 AA.
AC P97585;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 09, Last annotation update)
DE Dihydroethione-inducible gene-2 (Fragment).
GN DIG-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Murus
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FISHER 344;
RX MEDLINE=97122421; PubMed=8028041;
RA Primiano T., Gastel J.A., Kensler T.W., Surter T.P.;
RT "Isolation of cDNAs representing dihydroethione responsive genes.";
RL Carcinogenesis 17:2297-2303(1996).
DR EMBL: U66323; AAB3982.1; -
FT NON TER 79
SQ SEQUENCE 79 AA; 7999 MW; F45B17AFFA7390AF CRC64;

Query Match 100.0%; Score 20; DB 11; Length 39;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 5 VLEP 8

RESULT 24
Q01970
ID Q01970 PPELIMINARY; PPT; 80 AA.
AC Q01970;
DT 01-JUL-1997 (TReMBLrel. 04, Created)

```

```

DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Hypothetical 9.5 kDa protein.
GN M01D7.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998)
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX Gattung S., Goela D.;
RT "The sequence of C. elegans cosmid M01D7.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX Waterston R.;
RT "Direct Submission.";
RL Submitted (AUG 2001) to the EMBL/GenBank/DBJ databases.
DP EMBL: AF003739; AAB58066.1; -
KW Hypothetical protein.
SQ SEQUENCE 80 AA; 9457 MW; 70889FB8AAF87D0C CRC64;

Query Match 100.0%; Score 20; DB 5; Length 80;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 72 VLEP 75

RESULT 25
Q9QQ86
ID Q9QQ86 PPELIMINARY; PPT; 81 AA.
AC Q9QQ86;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Fusion protein (Fragment).
GN F.
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RA Fickel J., Czupalla O.;
RT "Canine distemper virus in a fox (Vulpes vulpes)";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF158979; AAB47562.1; -
DR InterPro: IPR000776; Fusion gly.
DE Flam, PF090523, fusion gly, 1.
FT NON TER 81
SQ SEQUENCE 81 AA; 8768 MW; 7791FF09B40DEB6B CRC64;

Query Match 100.0%; Score 20; DB 12; Length 81;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 36 VLEP 39

```

Search completed. March 5, 2003, 08:33:22  
Job time : 32 secs

GenCore version 5.1.3  
Copyright 1993-2003 Argonne LRI

DM protein - protein search, using sw model

Run on: March 5, 2003, 08:27:04, Search time 34 Seconds  
(without alignments)  
15 677 Million cell updates/sec

Title: US-09-732-411 15

Perfect score: 20

Sequences: 1 VLEP 4

Scoring table: BLAST/MSD

Gapop 10.0, Gapext 0.5

Searched: 90470 seqs, 13250620 residues

Total number of hits satisfying chosen parameters: 60470

Minimum DB seq length: 6  
Maximum IP seq length: 1000000

Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database: A Genbank 1010022

- 1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT
- 2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT
- 3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT
- 4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT
- 5: /SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT
- 6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT
- 7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT
- 8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT
- 9: /SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT
- 10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT
- 11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT
- 12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT
- 13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT
- 14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT
- 15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT
- 16: /SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT
- 17: /SID22/gcgdata/geneseq/geneseq-emb1/AA1996.DAT
- 18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT
- 19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT
- 20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT
- 21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT
- 22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT
- 23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	4	21 AAR28663	Chemotactic peptide
2	20	100.0	4	22 AAR29558	Adhesion-modulator
3	20	100.0	4	21 AAR28661	Chemotactic peptide
4	20	100.0	8	17 AAM06332	N-terminus of fec
5	20	100.0	8	17 AAR94654	Fragment of recept
6	20	100.0	9	16 AAR84629	Wheat acetyl-Coenz
7	20	100.0	10	20 AAY07164	HLA binding peptide
8	20	100.0	10	20 AAY07127	HLA binding peptide
9	20	100.0	14	22 AAM06563	Human transcription
10	20	100.0	17	21 AAR08085	Amino acid sequenc

11	20	100.0	17	21 AAR08086	Amino acid sequenc
12	20	100.0	19	19 AAW70175	Internal peptide f
13	20	100.0	19	22 AAS06633	Internal peptide f
14	20	100.0	20	22 AAR03346	Adhesion-related a
15	20	100.0	25	16 AAR79207	TGF-beta1 residues
16	20	100.0	25	19 AAR7273	Peptide #20 with c
17	20	100.0	26	15 AAR52310	Mouse heavy chain
18	20	100.0	27	22 AEB31072	Peptide #1723 enco
19	20	100.0	27	22 AEB36261	Peptide #1767 enco
20	20	100.0	27	22 AAR21633	Peptide #1632 enco
21	20	100.0	27	22 AAM57635	Human fibrin exper
22	20	100.0	27	22 AAM69425	Human bone marrow
23	20	100.0	27	22 AAM17353	Peptide #1733 enco
24	20	100.0	27	22 AAM29756	Peptide #1733 enco
25	20	100.0	27	22 AAM04961	Peptide #1633 enco
26	20	100.0	27	22 AAR03043	Human peptide enco
27	20	100.0	30	18 AAW24711	Finger 2 domain of
28	20	100.0	34	16 AAR66400	GalNAc-4-epitope
29	20	100.0	34	18 AAW16483	N-acetylglucosam
30	20	100.0	34	21 AAR92790	Yersinia faecalis IgF
31	20	100.0	34	21 AAY90551	Finger 2 subdomain
32	20	100.0	34	22 AAM96570	Human reticulocyte
33	20	100.0	35	21 AAY44142	Core polypeptide f
34	20	100.0	35	22 AAR03043	Peptide #1733 enco
35	20	100.0	35	22 ABB01977	Viral core polypep
36	20	100.0	35	22 AAM13050	Peptide #1633 enco
37	20	100.0	35	22 AAR77497	Core polypeptide f
38	20	100.0	36	21 AAB00613	Yersinia TGF-beta 5
39	20	100.0	37	22 ABB42603	Peptide #10109 eno
40	20	100.0	37	22 AAR03043	Peptide #1633 enco
41	20	100.0	37	22 AAR03043	Peptide #1633 enco
42	20	100.0	37	22 AAM76300	Human bone marrow
43	20	100.0	37	22 AAM36419	Peptide #10456 eno
44	20	100.0	37	22 AAR03043	Peptide #1633 enco
45	20	100.0	39	21 AAR03043	Peptide #1633 enco
46	20	100.0	40	22 AAM05085	Human polypeptide
47	20	100.0	42	22 ABE29320	Peptide #1633 enco
48	20	100.0	42	22 ABE29320	Peptide #1633 enco
49	20	100.0	43	22 AAR03043	Peptide #1633 enco
50	20	100.0	43	22 AAM05085	Human brain exper

ALIGNMENTS

RESULT 1

AA28663 standard, peptide; 4 AA.

AA28663:

AC AA28663:

DT 13-FEB 2001 (first entry)

DE Chemotactic peptide pepJ'

FW Chemotactic, osteopontin, vulnery, antiarthritic, anti-infectio;

KW cytostatic, antitumor, antiinflammatory, osteopathic;

KW wound healing; cell migration; chemotaxis; atherosclerosis; cancer;

KW angiogenic-associated disease; arthritis; psoriasis; haemangioma;

KW ocular neovascularisation; cell apoptosis; nitrous oxide production;

KW inflammation; osteoporosis; immune disease.

OS Mammalia.

OS Synthetic.

FN WC000063247 A2.

PD 26-OCT-2000.

PF 17-APP-2000; 2000WO-US10344.

PP 14-APP 1999; 99US 0129764

XX



XX Ashkar S;  
 XX WPI: 2000-687159/67  
 XX New osteopontin-derived chemotactic and inhibitory peptides, useful for  
 PT promoting scarless wound healing, modulating cellular chemotaxis,  
 PT treating formation of atherosclerotic plaques and preventing metastasis  
 XX  
 XX Claim 14; Page 42; 54pp; English.  
 XX The present sequence is an osteopontin-derived chemotactic peptide.  
 CC Such chemotactic peptides are useful for promoting scarless wound  
 CC healing, modulating chemotaxis and promoting cell migration to a target  
 CC site in a cell of a subject. They are also used for modulating cellular  
 CC chemotaxis in a mammalian cell such as smooth muscle cell, a macrophage,  
 CC an endothelial cell, a vascular cell and a tumorigenic cell. They are  
 CC useful for treating the formation of atherosclerotic plaques in a  
 CC subject. The peptides are used for preventing metastasis, treating an  
 CC angiogenic-associated disease such as arthritis, psoriasis, haemangioma,  
 CC tumour metastasis or ocular neovascularisation. They are also used for  
 CC activating cell apoptosis, for modulating nitrous oxide production and  
 CC for inducing chemotaxis. The peptides are useful for diagnosing, treating  
 CC and preventing tumour metastasis, inflammation, osteoporosis and immune  
 CC diseases. They can also be used to enhance an immune response by  
 CC attracting macrophages  
 XX  
 XX Sequence 6 AA;  
 Query Match 100.0%; Score 20; DB 21; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLEP 4  
 DB 2 VLEP 5  
 RESULT 4  
 ID AAW06132 standard; peptide; 8 AA  
 AC AAW06132  
 XX 17-JAN-1997 (first entry)  
 DT  
 DE N-terminus of receptor-type tyrosine kinase protein ligand  
 XX  
 XX Receptor type tyrosine kinase; ligand; coomassie staining, PAS staining,  
 KW N-terminus; human.  
 XX Homo sapiens.  
 XX JP08188596-A.  
 XX 23-JUL-1996.  
 XX 13-JAN 1995; 94JP 0001677.  
 XX 09-NOV-1994; 94JP 0275411.  
 PR 19-OCT-1994; 94JP 023484A  
 XX (ASAH ) ASAH FASEI KOKYO KK  
 XX WPI: 1996-388601/39.  
 XX New ligand for receptor type tyrosine kinase - has mol.wt. 22-25  
 PT kiloDalton(s) and is positive for Coomassie and PAS staining  
 XX Claim 3; Page 43; 51pp; Japanese.  
 XX This sequence represents the N-terminus of a receptor-type tyrosine

CC kinase receptor binding ligand of the invention (see AAW06133) and  
 CC AAW06134). The ligands of the invention recognise the fragment of the  
 CC receptor type kinase represented by AAW06130 (see AAW06131 for  
 CC full length sequence). The proteins of the invention have a molecular  
 CC weight of 23500 (plus or minus 1500) Da, and are positive for Coomassie  
 CC staining and PAS staining. The protein is a new ligand of receptor type  
 CC tyrosine kinases, and can be prepared by standard recombinant  
 CC techniques.  
 XX  
 XX Sequence 8 AA;  
 Query Match 100.0%; Score 20; DB 17; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLEP 4  
 DB 4 VLEP 7  
 RESULT 5  
 ID AAW94654 standard; Protein; 8 AA.  
 AC AAW94654;  
 XX 18 OCT-1996 (first entry)  
 DT  
 DE Fragment of receptor type tyrosine kinase (TK) ligand.  
 XX  
 XX Receptor type tyrosine kinase, TK, ligand; differentiation;  
 KW haematopoietic stem cell; tyrosine; bone marrow; leukaemia.  
 XX Homo sapiens.  
 XX WO9611212-A1.  
 XX 18-APR-1996.  
 XX 09-OCT-1995; 95WO-JP02069.  
 XX 22-DEC-1994; 94JP 0320712.  
 PR 07-OCT-1994; 94JP 0244433.  
 XX 20-OCT-1994; 94JP 0302882.  
 XX (ASAH ) ASAH FASEI KOKYO KK.  
 XX Ohno M, Sakano S;  
 XX WPI: 1996-209809/21.  
 XX Ligand peptide binding to receptor-type tyrosine kinase - enhances  
 PT intracellular tyrosine phosphorylation, useful for investigation of  
 PT undifferentiated blood cell behaviour  
 XX  
 XX Disclosure; Page 162; 193pp; Japanese.  
 XX A ligand polypeptide which binds to the extracellular part of a  
 CC specific receptor-type tyrosine kinase and induces phosphorylation  
 CC of tyrosine within the cell can be used in the study of the  
 CC differentiation of blood cells such as the haematopoietic stem  
 CC cells, of disease processes such as leukaemia, and of the biology of  
 CC bone marrow transplantation. The ligand plays a role in the  
 CC differentiation process and the specific ligand target is expressed  
 CC in undifferentiated blood cells.  
 XX  
 XX Sequence 8 AA;  
 Query Match 100.0%; Score 20; DB 17; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLEP 4

DB 4 VLEP 7  
 ||||  
 1 VLEP 4  
 2 VLEP 5

Best Local Similarity 100.0%; Pred. No. 7 aa-05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6  
 AAR84629  
 ID AAR84629 standard; Peptide; 9 AA.  
 XX AAR84629;  
 DT 02-JUN-1996 (first entry)  
 XX Wheat acetyl-Coenzyme A-carboxylase peptide sequence.  
 DE Acetyl Coenzyme A carboxylase; ACCase; plasmid pK11;  
 KW transgenic plant, modified oil content;  
 KW polyhydroxyalkanoate polymer; herbicide resistance;  
 KW monodict crop improvement  
 OS Triticum aestivum.  
 XX WO9529246-A1.  
 PN 02-NOV-1995.  
 XX 21-APR-1994; 94WO-GB00846.  
 PF 21-APR-1994; 94WO-GB00846.  
 PR (ZENE) ZENECA LTD.  
 PA Bright SWJ, Elborough KM, Pentem PA, Glasas AP;  
 PI WPI; 1995 192004/49  
 DR DNA encoding acetyl Coenzyme A carboxylase - used for developing  
 PT plants with controlled expression of ACCase, e.g. for controlling  
 PT fatty acid synthesis.  
 XX Disclosure; Fig 3; 61pp; English.  
 CC Wheat acetyl Coenzyme A carboxylase (ACCase) was partially  
 CC purified from wheat germ and a dominant 220 kDa band was identified  
 CC as ACCase by column chromatography and SDS-PAGE. After  
 CC purification in the gel, the protein was hydrolysed using  
 CC endoproteinase LysC, and resulting peptides were purified by  
 CC electrophoresis and loaded onto an Axi 477A pulse liquid  
 CC protein sequencer. Sequence data of 4 peptides (this peptide and  
 CC peptides AAR84625, AAR84627 and AAR84631) were compared with plasmid  
 CC pK11. Reduced amino acid sequences (AAR84630, AAR84636, AAR84638 and  
 CC AAR84632) so as to authenticate pK11 (see AAT04948) as wheat ACCase  
 CC partial cDNA. More specifically, this peptide corresponds to  
 CC amino acids 419-437 of the pK11 deduced AA sequence AAR84619.  
 CC (i.e. AAR84630). Partial cDNA clone pK11 (NCIF 40553) can be  
 CC used to create a sense/antisense expression cassette to  
 CC transform rape and other oilseed plants (canola, soybean,  
 CC sunflower) to downregulate production of the ACCase enzyme.  
 CC The transgenic plants have a lower or a modified oil content.  
 CC Down-regulation of oil synthesis can be used to divert the  
 CC substrate, acetyl Coenzyme A, into synthesis of alternative  
 CC storage materials (starch, protein or novel polymers e.g.  
 CC polyhydroxyalkanoates). Full-length ACCase clones can be used  
 CC to create transgenic plants over-expressing ACCase, and  
 CC therefore with increased oil content. ACCase over-expression in  
 CC transgenic plants such as wheat, barley, maize and rice, which are  
 CC normally sensitive to herbicides, results in  
 CC arylxyphenoxymethyl herbicide and alkylketone herbicide resistance in  
 CC the transgenic plants (dicots are normally resistant to these  
 CC herbicides).  
 XX Sequence 9 AA.

Query Match 100.0%; Score 20; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7  
 AAY07169  
 ID AAY07169 standard; Peptide; 10 AA.  
 XX AAY07169;  
 DT 02-JUN-1999 (first entry)  
 XX HLA binding peptide.  
 DE Cancer associated antigen; diagnosis; research; treatment; human;  
 KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;  
 KW prostate cancer.  
 XX Homo sapiens.  
 XX WO9904265-A2.  
 PN 28-JAN-1999.  
 PD 15-JUL-1998; 98WO-US14679.  
 PF 22-JUN-1999; 98US 0102322.  
 PP 17-JUL-1997; 97US-0896164.  
 PP 10-OCT-1997; 97US-0061539.  
 PP 10-OCT-1997; 97US-0061765.  
 PP 10-OCT-1997; 97US-0948705.  
 PP 11-OCT-1997; 97GR-0021697.  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 XX Chen Y, Gout I, Gure A, O'Hare M, Obata Y, Old LJ;  
 PI Pfeundschoh M, Sahin U, Scanlan MJ, Stockert E;  
 PI Tureci O;  
 XX WPI; 1999-132448/11.  
 DR New isolated cancer associated nucleic acids and polypeptides -  
 PT isolated using sera from cancer patients, used to develop products  
 PT for the diagnosis, monitoring or treatment of cancers  
 XX Example 16; Page 762; 787pp; English  
 PS The invention relates to a method for diagnosing a disorder characterised  
 CC by expression of a human cancer associated antigen precursor coded for by  
 CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a  
 CC biological sample isolated from a subject with an agent that specifically  
 CC binds to the NAM, an expression product or a fragment of an expression  
 CC product complexed with an RNA molecule; and (b) determining the  
 CC interaction between the agent and the NAM or the expression product as a  
 CC determination of the disorder. The products and methods can be used in  
 CC the diagnosis, monitoring, research, or treatment of conditions  
 CC characterised by the expression of various cancer associated antigens.  
 CC The invention provides nucleic acid sequences and encoded polypeptides  
 CC which are cancer associated antigen precursors expressed in human breast  
 CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and  
 CC lung cancer  
 XX Sequence 10 AA;

Query Match 100.0%; Score 20; DB 20; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4



```

Db      5 VLEP 8
|||||
RESULT 8
AAV07127
ID AAY07127 standard; Peptide; 10 AA
XX
AC AAY07127;
XX
DE 02-JUL-1999 (first entry)
XX
DE HLA binding peptide.
XX
KW Cancer associated antigen, diagnosis, research, treatment; human;
KW breast cancer; colon cancer, gastric cancer, lung cancer;
KW prostate cancer.
XX
OS Homo sapiens.
XX
PN W09904265-A2.
XX
PD 28 JAN-1999.
XX
PF 15-JUL-1998; 98WO-US14679.
XX
PR 22 JUN 1998; 98US 0102322.
PR 17-JUL-1997; 97US-0896164.
PR 10-OCT-1997; 97US-0061599.
PR 10-OCT-1997; 97US-0061765.
PR 10-OCT-1997; 97US-0948705.
PR 11-OCT-1997; 97GB-0007597.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
XX
PI Chen Y, Gout I, Gatt A, O'Hare M, Ohta Y, Old LJ;
PI Pfeleuschuh M, Sahin U, Scanlan MJ, Stockert R;
PI Tureci O;
XX
DR WPI; 1999-132448/11.
XX
PT New isolated cancer associated nucleic acids and polypeptides.
PT isolated using sera from cancer patients, used to develop products
PT for the diagnosis, monitoring or treatment of cancers
XX
PS Example 16; Page 765; 787pp; English.
XX
CC The invention relates to a method for diagnosing a disorder characterised
CC by expression of a human cancer associated antigen precursor coded for by
CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a
CC biological sample isolated from a subject with an agent that specifically
CC binds to the NAM, an expression product or a fragment of an expression
CC product complexed with an HLA molecule; and (b) determining the
CC interaction between the agent and the NAM or the expression product as a
CC determination of the disorder. The products and methods can be used in
CC the diagnosis, monitoring, research, or treatment of conditions
CC characterised by the expression of various cancer associated antigens.
CC The invention provides nucleic acid sequences and encoded polypeptides
CC which are cancer associated antigen precursors expressed in human breast
CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
CC lung cancer.
XX
SQ Sequence 10 AA;
Query Match 100 %, Score 20; PR 20; Length 10;
Best Local Similarity 100 %; Pled No 90;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLEP 4
|||
Db 5 VLEP 8

RESULT 9
AAM00583
ID AAM00583 standard; Peptide; 14 AA.
XX
AC AAM00583;
XX
DE 01-OCT-2001 (first entry)
XX
DE Human transcription factor fragment SEQ ID NO: 1131.
XX
KW Human, single nucleotide polymorphism, SNP, paternity test;
KW forensic test; aberrant protein expression.
XX
OS Homo sapiens.
XX
PI W000001570 A2
XX
PD 19-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US00322.
XX
PP 07-JAN 2000; 2000US 0174962.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Leach MD;
XX
DR WPI, 2001-451871/48.
DR N-PSDB; AAH89700.
XX
XX
PT Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
PT infection and diabetes.
XX
PS Disclosure; Page 427; 475pp; English.
XX
CC The present invention relates to human nucleic acids containing single
CC nucleotide polymorphisms (SNPs). These can be used in forensic and
CC paternity tests, and to aid in the treatment of diseases associated with
CC aberrant protein expression, including cancer, amyloidosis, diabetes,
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,
CC meningitis, muscular disorders, dementia, neurological diseases, tubercous
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC autoimmunity. The present sequence is a peptide encoded by a
CC polymorphism-containing oligonucleotide fragment of the invention.
XX
SQ Sequence 14 AA,
Query Match 100 %, Score 20; PR 20; Length 14;
Best Local Similarity 100 %; Pled No 13e02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLEP 4
|||
Db 5 VLEP 8

RESULT 10
AAB08085
ID AAB08085 standard; peptide; 17 AA.
XX
AC AAB08085;
XX
DE 24 DEC-2000 (first entry)
XX
DE Amino acid sequence of a helper T cell epitope from CDV.
XX
KW T helper cell epitope; CDV; immune response; Canine vaccine.
XX
OS Canine distemper virus.

```

```

PN WC200046390-A1.
XX
XX 10-AUG-2000.
XX
XX 07-FEB-2000; 2000WQ-AU000070
XX
XX 05-FEB-1999; 99AU-0008533.
XX 04-AUG-1999; 99AU-0002013.
XX
XX (UYME ) UNIV MELBOURNE.
XX (CSIC-) CSL LTD.
XX (CSIP ) COMMUNHEALTH SCI & IND RES ORG.
XX (CCCN ) COUNCIL QUEENSLAND INST MEDICAL RES.
XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
XX Jackson DC, Souravi G, Walker J;
PI
XX
XX WPI, 2000-532904/48.
XX
XX Novel T helper cell epitopes derived from canine distemper virus useful
XX for preparation of canine vaccines -
XX
XX Claim 1, Page 28; 54pp; English.
XX
XX AAB08076-B08101 represent T helper cell epitopes, derived from canine
XX distemper virus (CDV). Compositions comprising these T cell helper
XX epitopes are useful for inducing an immune response in an animal. The
XX epitopes are useful as components of animal, in particular, canine
XX vaccines, either simply as synthetic peptide based vaccines and as
XX additions to vaccines containing more complex antigens.
XX
XX Sequence 17 AA;
SQ
Query Match 100.0%; Score 20; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLEP 4
DB 6 VLEP 9
|||||
RESULT 12
AAW70175
ID AAW70175 standard; peptide; 19 AA.
XX
XX AAW70175;
XX
XX 07-DEC-1998 (first entry)
XX
XX Internal peptide fragment of CFP 9.
XX
XX Culture filtrate protein; CFP, H37RV, 2-D PAGE, electrophoretic, trypsin;
XX C18 capillary reversed phase chromatography; hemology; antigen; antibody;
XX human immunodeficiency virus; HIV.
XX
XX Mycobacterium tuberculosis.
XX
XX WO9829132-A1.
XX
XX 09-JUL-1998.
XX
XX 29-DEC-1997; 97WO-US24189.
XX
XX 31-DEC-1995; 95US-0034003
XX (UYNY ) UNIV NEW YORK STATE.
XX
XX Belisle JT, Laal S, Zolla-Pazner S,
XX
XX WPI; 1998-187787/13
XX
XX Early detection of mycobacterial infection - by testing a biological
XX fluid sample from a subject for the presence of anti-316s reactive
XX with Mycobacterium tuberculosis antigens
XX
XX Example 5; Page 88; 170pp; English.
XX
XX Sequences AAW70167-W70179 are internal peptide fragments of selected
XX culture filtrate proteins (CFPs) of M. tuberculosis (Mt), strain H37RV,
XX determined by LC MS-MS analysis. To obtain these sequences, the
XX proteins were resolved by 2-D PAGE, transferred to a membrane by
XX electroblotting, stained, destained, subjected to in-gel proteolytic
XX digestion with trypsin, and then eluted and separated by C18 capillary
XX reversed phase chromatography. These antigens and antibodies that form
XX against them can be used for the early detection of mycobacterial
XX disease, particularly in subjects infected with human immunodeficiency
XX virus (HIV).
XX
XX Sequence 19 AA;
SQ

```

Query Match 100.0%; Score 20; Pr 19; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEP 4  
 DB 15 VLEP 18

RESULT 13  
 ID AAE05631 standard; peptide; 19 AA.  
 AC AAE05631;  
 XX 24-SEP-2001 (first entry)  
 DE Internal peptide fragment #9 of Mycobacterium tuberculosis protein IT-42.  
 XX Mycobacterial disease, infection, 88 kDa protein, tuberculosis, TP,  
 KW liquid chromatography-mass spectrometry-mass spectrometry; LC-MS-MS;  
 KW culture filtrate protein; GFP; H37Rv; early antigen, serodiagnosis,  
 KW human immunodeficiency virus; HIV; protein IT 42.  
 XX Mycobacterium tuberculosis.  
 OS US6245331-B1.  
 PN 12-JUN-2001.  
 PD 31-DEC-1997; 97US-0001984.  
 PF 02-JAN-1997; 97US-0034003.  
 PR (UNNY-) UNIV NEW YORK MEDICAL CENT.  
 PA (COLS) UNIV COLORADO STATE.  
 XX Laal S, Zolla-Pazner S, Belisle JT;  
 WPI; 2001-424324/45.  
 DR Detecting a mycobacterial disease (tuberculosis) in individuals  
 PT comprise assaying a biological sample for the presence of  
 PT anti-Mycobacterium tuberculosis antibodies or M. tuberculosis  
 PT antigen-antibody complex -  
 XX Example 5, Column 55-56; 36pp; English.  
 PS The present invention relates to a method for early detection of active  
 CC mycobacterial disease or infection comprises assaying a biological fluid  
 CC sample for the presence of early antibodies specific for an 88-kDa  
 CC Mycobacterium tuberculosis (Mt) protein or immune complexes consisting of  
 CC an 88-kDa M. tuberculosis protein antigen complexed with an antibody  
 CC specific for the antigen. The method is useful for the early and rapid  
 CC detection of mycobacterial disease, particularly tuberculosis, in  
 CC individuals at heightened risk of developing tuberculosis. This  
 CC individuals include human immunodeficiency virus (HIV)-infected subjects  
 CC or other immunocompromised individuals. The method is a rapid and  
 CC inexpensive screening procedure for detecting mycobacterial disease.  
 CC The present sequence is an internal peptide fragment of M. tuberculosis  
 CC protein IT-42. The N-terminal peptide or internal peptide fragment is  
 CC identified by liquid chromatography-mass spectrometry-mass spectrometry  
 CC (LC-MS-MS) of selected Mt culture filtrate proteins (CFPs) of Mt H37Rv  
 CC early antigen, used in the exemplification of the invention. The H37Rv  
 CC early antigen is used in the serodiagnosis of tuberculosis (TB).  
 XX Sequence 19 AA;

Query Match 100.0%; Score 20; Pr 22; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEP 4  
 DB 15 VLEP 18

RESULT 14  
 ID AAB50346 standard; peptide; 20 AA.  
 AC AAB50346;  
 XX 09-MAR-2001 (first entry)  
 DE Adeno-associated virus capsid immunogenic peptide #4.  
 XX Adeno-associated virus; AAV; capsid; virus binding inhibition;  
 KW competitive inhibitor; immunogen; epitope.  
 XX Mastadenovirus.  
 OS W03067331F A2  
 PW 07 DEC 2000.  
 XX 20-MAY-2000; 2000WO-US14466  
 PF 28-MAY-1999; 99US-0321599.  
 PP (CELL-) CELL GENESYS INC.  
 PA Patel S, McArthur J;  
 WPI; 2001-061507/07  
 DR New polypeptide portion of a virus protein binding to an antibody  
 PT specific for the virus useful for inhibiting binding of the virus to a  
 PT cell or for binding host antibody to provide a transient tolerant or  
 PT non-responsive state -  
 XX Disclosure; Fig 4; 33pp; English.  
 PS The present sequence is given in a specification relating to  
 CC polypeptide portions of a virus protein or its derivative, that bind to  
 CC an antibody specific for the virus or inhibit binding of the virus to a  
 CC cell. The polypeptides are used in inhibiting the binding of viruses to  
 CC cells of a host. Oligopeptides that inhibit binding of virus to  
 CC receptor can be used as competitive inhibitors to release bound virus  
 CC in an adsorption-type assay, and if an antibody was used as an  
 CC immunoadsorbent, the oligopeptide could be used to elute bound virus  
 CC from a solid support to which virus antibody is immobilized. These  
 CC oligopeptides may further be used to bind to host antibody to provide a  
 CC transient tolerant or non-responsive state.  
 XX Sequence 20 AA;

Query Match 100.0%; Score 20; Pr 22; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEP 4  
 DB 13 VLEP 16

RESULT 15  
 ID AAR79207 standard; peptide; 25 AA.  
 AC AAR79207;  
 XX 06-MAR-1996 (first entry)  
 DE TGF-beta5 residues 358-382.



CC Modification of a rodent antibody or fragment by resurfacing in order  
 CC to produce a humanised rodent antibody can be determined by calculating  
 CC homology between murine and human antibody surfaces. In order to test  
 CC the resurfacing approach of the invention, three humanisation  
 CC experiments were set up: (1) traditional loop grafting, (2) resurfacing  
 CC approach using most similar chain, and (3) resurfacing approach using  
 CC human sequences with most similar surface residues. AAP52243-447 are the  
 CC surface residue patterns in mouse heavy chain antibody variable regions.  
 CC These "patches" were used in the third method, where rodent light and  
 CC heavy chains were matched and the most similar human sequence found  
 CC independently only over the surface residues indicated in AAP52030-67.

XX SQ Sequence 26 AA;

Query Match 100.0% Score 26; DB 15; Length 26;  
 Best Local Similarity 100.0%; Pred No. 250402; Indels 0; Gaps 0;  
 Matches 4; Conservation 0; Mismatches 0;

OY 1 VLEP 4  
 ||||  
 Db 5 VLEP 8

RESULT 19  
 ABB31072  
 ID ABB31072 standard; Peptide; 27 AA.

XX AC ABB31072;

DT 01-FEB-2002 (first entry)

DE Peptide #3723 encoded by breast cell single exon nucleic acid probe.

XX Human; microarray; single exon probe; gene expression; breast,  
 KW disease; cancer.

XX OS Homo sapiens.

XX PN WO200157271-A2.

XX PD 09-AUG-2001;

XX PF 30-JAN-2001, 2001WO-0500662

XX PP 04-FEB-2000; 2000US-0180112

XX PP 26 MAY 2000; 2000US-0207456

XX PP 30-JUN-2000; 2000US-0609409

XX PP 03-AUG-2000; 2000US-0632366

XX PP 21-SEP-2000; 2000US-0234687

XX PP 27-SEP-2000; 2000US-0236359.

XX PP 04-OCT-2000; 2000EP-0034263

XX (MOLECULAR DYNAMICS INC)

XX PA Penn SG, Hanzel DK, Chen W, Rank DP;

XX PI WPI; 2001-496933/54.

XX PT New spatially addressable set of single exon nucleic acid probes,  
 PT useful for measuring gene expression in sample derived from human  
 PT breast, comprises number of single exon nucleic acid probes -

XX PS Claim 27, SEQ ID NO 14440, 327p + sequence listing, English.

XX The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human breast and BT 474 cells. The method involves contacting  
 CC the probes with a collection of detectably labelled nucleic acids  
 CC derived from mRNA of human breast, and then measuring the label  
 CC bound to each probe of the microarray. The probes are useful for  
 CC verifying the expression of regions of genomic DNA predicted to  
 CC encode proteins. They are useful for gene discovery, and for  
 CC determining predisposition and/or prognosing breast disease. Gene

CC expression analysis is useful for assessing the toxicity of chemical  
 CC agents on cells. The microarray of this invention presents a far greater  
 CC diversity of probes for measuring gene expression, with far fewer than  
 CC than expressed sequence tag microarrays. The method is suitable for  
 CC rapid production of functional information from genomic sequence. The  
 CC present sequence is a peptide encoded by a single exon nucleic acid  
 CC probe of the invention.

CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pat\_sequences.

XX SQ Sequence 27 AA;

Query Match 100.0% Score 20; DB 22; Length 27;  
 Best Local Similarity 100.0%; Pred No. 256402; Indels 0; Gaps 0;  
 Matches 4; Conservation 0; Mismatches 0;

OY 1 VLEP 4  
 ||||  
 Db 20 VLEP 23

RESULT 19

ABB36261  
 ID ABB36261 standard; Peptide; 27 AA.

XX AC ABB36261;

DT 04-FEB-2002 (first entry)

DE Peptide #3767 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

XX OS Homo sapiens.

XX PN WO200157277-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001, 2001WO-0500662.

XX PP 04-FEB-2000; 2000US-0180112.

XX PP 26 MAY 2000; 2000US-0207456.

XX PP 30-JUN-2000; 2000US-0609409.

XX PP 03-AUG-2000; 2000US-0632366.

XX PP 21-SEP-2000; 2000US-0234687.

XX PP 27-SEP-2000; 2000US-0236359.

XX PP 04-OCT-2000; 2000EP-0034263.

XX (MOLECULAR DYNAMICS INC)

XX PA Penn SG, Hanzel DK, Chen W, Rank DP;

XX PI WPI; 2001-483447/52.

XX PT Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human foetal liver -

XX PS Claim 27, SEQ ID NO 28806, 630pp + sequence listing, English.

XX The invention relates to a single exon nucleic acid probe for  
 CC measuring human gene expression in a sample derived from human foetal  
 CC liver. The single exon nucleic acid probes may be used for predicting,  
 CC measuring and displaying gene expression in samples derived from human  
 CC foetal liver. The present sequence is a peptide encoded by a single exon  
 CC nucleic acid probe of the invention.

CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pat\_sequences.

XX SQ Sequence 27 AA;

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Query Match      100.0%; Score 20; DB 22; Length 27;
Best Local Similarity 100.0%; Pred No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 VLEP 4
DB 20 VLEP 23

RESULT 20
ABB21633
ID ABB21633 standard; Protein: 27 AA.
XX
AC ABB21633;
XX
DT 23 JAN-2002 (first entry)
XX
DE Protein #3612 encoded by probe for measuring heart cell gene expression
XX
KW Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.
XX
CS Homo sapiens.
XX
XX WQ200157275-A2.
XX
PD 09-AUG-2001.
XX
PP 30 JAN 2001; 2001WO 0500666.
XX
PP 04 FEB 2000; 2000US 0180312.
XX
PP 06 MAY 2000; 2000US 0207456.
XX
PP 30 JUN 2000; 2000US 0608408.
XX
PP 02 AUG 2000; 2000US 0633366.
XX
PP 21 SEP 2000; 2000US 0234487.
XX
PP 27 SEP 2000; 2000US 0236359.
XX
PP 04 OCT 2000; 2000US 0234263.
XX
PA (MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DP;
XX
XX WPI, 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
XX
PS Claim 15, SEQ ID No 23403; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO
CC at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 27 AA;
Query Match      100.0%; Score 20; DB 22; Length 27;
Best Local Similarity 100.0%; Pred No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 VLEP 4
DB 20 VLEP 23

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RESULT 21
AAM57035
ID AAM57035 standard; Protein: 27 AA.
XX
AC AAM57035;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 29140.
XX
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer.
XX
CS Homo sapiens.
XX
XX WQ200157275-A2.
XX
PD 09-AUG-2001.
XX
PP 30 JAN 2001; 2001WO 0500667.
XX
PP 04 FEB 2000; 2000US 0180312.
XX
PP 06 MAY 2000; 2000US 0207456.
XX
PP 30 JUN 2000; 2000US 0608408.
XX
PP 02 AUG 2000; 2000US 0633366.
XX
PP 21 SEP 2000; 2000US 0234487.
XX
PP 27 SEP 2000; 2000US 0236359.
XX
PP 04 OCT 2000; 2000US 0234263.
XX
PA (MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DP;
XX
XX WPI, 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
PS Example 4; SEQ ID NO. 29140; 650pp + Sequence Listing, English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention.
XX
SQ Sequence 27 AA;
Query Match      100.0%; Score 20; DB 22; Length 27;
Best Local Similarity 100.0%; Pred No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 VLEP 4
DB 20 VLEP 23

RESULT 22
AAM69425
ID AAM69425 standard; Protein: 27 AA.
XX
AC AAM69425;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed probe encoded protein SEQ ID NO. 29731.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma.

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XX OS Homo sapiens.
XX PN W0200157276-A2.
XX XX
XX PD 09 AUG-2001.
XX PF
XX PF 30-JAN-2001; 2001WO-US006688.
XX PR 04 FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21 SEP-2000; 2000US-0334687.
XX PR 27-SEP-2000; 2000US-0336359.
XX PR 04-OCT-2000; 2000GB-0024363.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Pank DR;
XX DR WPI; 2001-488900/53.
XX XX
XX PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human bone marrow.
XX PS Example 4; SEQ ID NO: 29731; 658bp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX samples, which may enable the improved diagnosis and treatment of cancers
XX such as lymphoma, leukaemia and myeloma. The present sequence is a
XX protein encoded by one of the probes of the invention.
XX SQ Sequence 27 AA;
XX
XX Query March 100.0%; Score 20; DB 22; Length 27;
XX Best Local Similarity 100.0%; Pred. No. 2 60.02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 VLEP 4
XX DB 20 VLEP 23
XX
XX RESULT 23
XX AAM17259
XX ID AAM17259 standard; Protein; 27 AA.
XX AC AAM17259;
XX XX
XX DT 12-OCT-2001 (first entry)
XX DE Peptide #3693 encoded by probe for measuring cervical gene expression.
XX KW Probe; human; microarray; gene expression; cervical epithelial cell;
XX KW Cervical cancer
XX OS Homo sapiens
XX PN W0200157276-A2
XX XX
XX PD 09-AUG-2001
XX PF
XX PF 30-JAN-2001; 2001WO-US006688.
XX PR 04 FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21 SEP-2000; 2000US-0334687.
XX PR 27-SEP-2000; 2000US-0336359.

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PP 04-OCT-2000; 2000GB-0024363.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Pank DR;
XX DR WPI; 2001-488901/53.
XX XX
XX PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells
XX PS Claim 27; SEQ ID NO: 22895; 487bp; English.
XX CC The present invention relates to a human single exon nucleic acid probe
XX (SNP) see AAL10098 AAL10490. The present sequence is a peptide encoded
XX by the such probe. The SNPs are derived from human Heli cells. The SNPs
XX can be used to produce a single exon microarray, which can be used for
XX measuring human gene expression in a sample derived from human cervical
XX epithelial cells. By measuring gene expression, the probes are therefore
XX useful in grading and/or staging of diseases of the cervix, notably
XX cervical cancer.
XX CC Note: the sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from Wipo
XX at ftp.wipo.int/pub/published_per_sequences
XX SQ Sequence 27 AA;
XX
XX Query March 100.0%; Score 20; DB 22; Length 27;
XX Best Local Similarity 100.0%; Pred. No. 2 60.02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 VLEP 4
XX DB 20 VLEP 23
XX
XX RESULT 24
XX AAM29756
XX ID AAM29756 standard; Protein; 27 AA.
XX AC AAM29756;
XX XX
XX DT 17-OCT-2001 (first entry)
XX DE Peptide #3793 encoded by probe for measuring placental gene expression.
XX KW Probe; microarray; human; placenta; antenatal diagnosis;
XX KW genetic disorder.
XX OS Homo sapiens
XX PN W0200157272-A2.
XX XX
XX PD 09-AUG-2001.
XX PF
XX PF 30-JAN-2001; 2001WO-US006683.
XX PR 04 FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21 SEP-2000; 2000US-0334687.
XX PR 27-SEP-2000; 2000US-0336359.
XX PR 04 OCT 2000; 2000GB-0024363.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Pank DR;
XX DR WPI; 2001-488997/53.
XX XX
XX PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta.

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XX PS Claim 27; SEQ ID NO 30025; 654pp, English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP;
CC see AA131315-AA157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders.
XX
SQ Sequence 27 AA;
    Query Match 100.0%; Score 20; DB 22; Length 27;
    Best Local Similarity 100.0%; Pred No 2; Seq 0;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 1 VLEP 4
    Db 20 VLEP 23

RESULT 25
AAM04951
ID AAM04951 standard; Protein; 27 AA.
XX
AC AAM04951;
XX
DT 09-OCT-2001 (first entry)
XX
DE Peptide #3633 encoded by probe for measuring breast gene expression.
XX
KW Probe, human, breast disease; breast cancer; development disorder;
KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
OS Homo sapiens.
XX
PN NC020157270.A2.
XX
PD 09-AUG-2001.
XX
PF 20-JAN-2001; 2001WG-US00661.
XX
PR 04-FEB-2000; 2000US 0180312.
PR 26-MAY-2000; 2000US 0207456.
PR 30-JUN-2000; 2000US-0608408
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US 0234587.
PR 27-SEP-2000; 2000US 0236359.
PR 04-OCT-2000; 2000JB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DP;
XX
WI: 2001-476286/51.
XX
PT Novel single exon nucleic acid probe used to measuring gene expression
PT in a human breast -
XX
PS Claim 27, SEQ ID NO 13691; 322pp; English.
XX
CC The present invention relates to novel single exon nucleic acid probes
CC (see AA100010-AA110067). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for measuring human gene expression in
CC a human breast sample, where the probe hybridises at high stringency to a
CC nucleic acid expressed in the human breast. The probes are useful for
CC predicting, diagnosing, grading, staging, monitoring and prognosing
CC diseases of the human breast, particularly those diseases with polygenic
CC aetiology. The diseases include: breast cancer; disorders of development,
CC inflammatory diseases of the breast; fibrocystic changes; proliferative
CC breast disease and non-carcinoma tumours.
CC Note. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO

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CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 27 AA;

Query Match 100.0%; Score 20; DB 22; Length 27;  
Best Local Similarity 100.0%; Pred No 2; Seq 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4

Db 20 VLEP 23

Search completed March 5, 2003, 08:32:09  
Job time : 35 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: Match 5, 2003, 08:33:25 ; Search time 13 Seconds  
(without alignments)  
12.975 Million full updates/sec

Title: US-09-732-411-15

Perfect score: 20

Sequence: 1 VLEP 4

Scoring table: BLASTW2  
Gap: 16.0, Gapov: 0.0

Searched: 18454 seqs, 42170167 residues

Total number of hits satisfying chosen parameters: 18454

Minimum DB seq length: 0

Maximum DB seq length: 100000000

Post-processing: Minimum Match 0%

Listing first 50 summaries

Database: Published Applications AA:

- 1: /cgn2\_6/prodata/1/pubaa/us06\_NEW\_PUB\_PEP\*
- 2: /cgn2\_6/prodata/1/pubaa/PCT\_NEW\_PUB\_PEP\*
- 3: /cgn2\_6/prodata/1/pubaa/US06\_NEW\_PUB\_PEP\*
- 4: /cgn2\_6/prodata/1/pubaa/US06\_PUBCOMB\_PEP\*
- 5: /cgn2\_6/prodata/1/pubaa/US07\_NEW\_PUB\_PEP\*
- 6: /cgn2\_6/prodata/1/pubaa/US07\_PUBCOMB\_PEP\*
- 7: /cgn2\_6/prodata/1/pubaa/PCTUS\_PUBCOMB\_PEP\*
- 8: /cgn2\_6/prodata/1/pubaa/us08\_PUBCOMB\_PEP\*
- 9: /cgn2\_6/prodata/1/pubaa/us09\_NEW\_PUB\_PEP\*
- 10: /cgn2\_6/prodata/1/pubaa/us09\_PUBCOMB\_PEP\*
- 11: /cgn2\_6/prodata/1/pubaa/US10\_NEW\_PUB\_PEP\*
- 12: /cgn2\_6/prodata/1/pubaa/US10\_PUBCOMB\_PEP\*
- 13: /cgn2\_6/prodata/1/pubaa/US10\_NEW\_PUB\_PEP\*
- 14: /cgn2\_6/prodata/1/pubaa/US10\_PUBCOMB\_PEP\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No	Score	Query %	Match	Length	EB	ID	Description
1	20	100.0	4	10	US-09-729-873-16		Sequence 16, Appl
2	20	100.0	4	10	US-09-732-411-15		Sequence 15, Appl
3	20	100.0	4	10	US-09-729-873-14		Sequence 14, Appl
4	20	100.0	7	9	US-09-998-909-11		Sequence 11, Appl
5	20	100.0	10	9	US-10-153-744-7		Sequence 7, Appl
6	20	100.0	26	9	US-09-956-236A-21		Sequence 21, Appl
7	20	100.0	27	10	US-09-864-761-16911		Sequence 36931, A
8	20	100.0	28	10	US-09-920-557-45		Sequence 45, Appl
9	20	100.0	37	10	US-09-864-761-41244		Sequence 41244, A
10	20	100.0	42	10	US-09-864-761-35819		Sequence 35819, A
11	20	100.0	44	9	US-09-925-299-784		Sequence 784, Appl
12	20	100.0	44	10	US-09-925-299-784		Sequence 784, Appl
13	20	100.0	47	10	US-09-864-761-46702		Sequence 46702, A
14	20	100.0	48	10	US-09-205-658-174		Sequence 174, Appl
15	20	100.0	49	10	US-09-864-761-40223		Sequence 40223, A
16	20	100.0	52	10	US-09-864-761-37977		Sequence 37977, A
17	20	100.0	53	10	US-09-864-761-44895		Sequence 44895, A
18	20	100.0	56	10	US-09-925-100-1385		Sequence 1385, Appl
19	20	100.0	61	10	US-09-864-761-34903		Sequence 34903, A

20	20	100.0	63	10	US-09-864-761-43309	Sequence 43309, A
21	20	100.0	65	8	US-09-808-031A-17	Sequence 17, Appl
22	20	100.0	65	10	US-09-864-761-35828	Sequence 35828, A
23	20	100.0	66	10	US-09-864-761-45067	Sequence 45067, A
24	20	100.0	67	10	US-09-864-761-48913	Sequence 48913, A
25	20	100.0	68	10	US-09-926-101-1620	Sequence 1620, Appl
26	20	100.0	70	10	US-09-864-761-39864	Sequence 39864, A
27	20	100.0	73	9	US-09-796-894-13221	Sequence 13221, Appl
28	20	100.0	77	10	US-09-864-761-42221	Sequence 42221, A
29	20	100.0	77	10	US-09-864-761-48627	Sequence 48627, A
30	20	100.0	78	10	US-09-925-297-752	Sequence 752, Appl
31	20	100.0	85	10	US-09-893-737-158	Sequence 158, Appl
32	20	100.0	88	10	US-09-925-297-1523	Sequence 1523, Appl
33	20	100.0	91	9	US-10-002-974-25	Sequence 25, Appl
34	20	100.0	91	10	US-09-864-761-33616	Sequence 33616, A
35	20	100.0	91	10	US-09-864-761-34143	Sequence 34143, A
36	20	100.0	91	10	US-09-864-761-34143	Sequence 34143, A
37	20	100.0	92	9	US-09-252-089-12	Sequence 12, Appl
38	20	100.0	101	9	US-09-738-626-4931	Sequence 4931, Appl
39	20	100.0	101	10	US-09-216-393-114	Sequence 114, Appl
40	20	100.0	101	10	US-09-216-393-114	Sequence 114, Appl
41	20	100.0	102	9	US-09-796-692-773	Sequence 773, Appl
42	20	100.0	102	10	US-09-924-359-32	Sequence 32, Appl
43	20	100.0	103	10	US-09-843-132-521	Sequence 521, Appl
44	20	100.0	107	10	US-09-864-761-34750	Sequence 34750, A
45	20	100.0	108	9	US-10-230-163-10	Sequence 10, Appl
46	20	100.0	108	9	US-10-230-163-10	Sequence 10, Appl
47	20	100.0	112	10	US-09-764-864-1249	Sequence 1249, Appl
48	20	100.0	114	10	US-09-911-284-149	Sequence 149, Appl
49	20	100.0	114	10	US-09-911-284-149	Sequence 149, Appl
50	20	100.0	117	10	US-09-764-864-1249	Sequence 1249, Appl

## ALIGNMENTS

### RESULT 1

US 09 729-873-16  
Sequence 16, Application US/09729873  
Parent No. US20010016421A1  
GENERAL INFORMATION:  
APPLICANT: Samy Ashkar  
TITLE OF INVENTION: Estrogen In Derived Chemotactic and Inhibitory Agents  
FILE REFERENCE: CMZ-123CP  
CURRENT APPLICATION NUMBER: US/09/729,873  
PCT FILING DATE: 2000-12-05  
PRIORITY APPLICATION NUMBER: 60/129,764  
PRIOR FILING DATE: 1999-04-15  
PRIOR APPLICATION NUMBER: PCT/US00/10344  
PRIOR FILING DATE: 2000-04-17  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 16  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: Cytokine  
US-09-729-873-16

Query Match: 100.0% Score 20; DB 10; Length 4;  
Best Local Similarity: 100.0%, Pred. No. 1.6e-05;  
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 VLEP 4

DB 1 VLEP 4

### RESULT 2

US 09 732-411-15

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; Sequence 15, Application US/09732411
; Patent No. US2000025823A1
; GENERAL INFORMATION:
; APPLICANT: Samy Ashkar
; TITLE OF INVENTION: Adhesion Modulatory Peptides and Methods for Use
; FILE REFERENCE: SME 124CF
; CURRENT FILING DATE: 2000-12-07
; PRIOR FILING DATE: 2000-04-16
; PRIOR APPLICATION NUMBER: US/09732,411
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: PCT/US00/10429
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 15
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-732-411-15

Query Match 100.0%; Score 20; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 VLEP 4
Db 1 VLEP 4

RESULT 3
US-09-729-873-14
; Sequence 14, Application US/09729873
; Patent No. US200003032A1
; GENERAL INFORMATION:
; APPLICANT: Samy Ashkar
; TITLE OF INVENTION: Correspondin Derived Chemotactic and Inhibitory Agents
; FILE REFERENCE: CM3 123CF
; CURRENT FILING DATE: 2000 12-05
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PCT/US00/10344
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-729-873-14

Query Match 100.0%; Score 20; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 VLEP 4
Db 2 VLEP 5

RESULT 4
US-09-998-909-11
; Sequence 11, Application US/09998909
; Patent No. US200016466A1
; GENERAL INFORMATION:
; APPLICANT: Hlavaty, John
; APPLICANT: Briggman, Joseph
; TITLE OF INVENTION: Detection and Treatment of Prostate Cancer
; FILE REFERENCE: WTP-027
; CURRENT APPLICATION NUMBER: US/09/998,909
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 62/250,294
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 3.0
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-998-909-11

Query Match 100.0%; Score 20; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 VLEP 4
Db 1 VLEP 4

RESULT 5
US-10-153-344-7
; Sequence 7, Application US/10153344
; Publication No. US20030004124A1
; GENERAL INFORMATION:
; APPLICANT: ROTHMAN, JOEL
; APPLICANT: BLOSS, TIM
; APPLICANT: WITZE, ERIC
; TITLE OF INVENTION: BTF3, AN INHIBITOR OF APOPTOSIS
; FILE REFERENCE: 407T-300410US
; CURRENT APPLICATION NUMBER: US/10/153,344
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 62/292,559
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10)-(10)
; OTHER INFORMATION: X is any amino acid
US-10-153-344-7

Query Match 100.0%; Score 20; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 VLEP 4
Db 6 VLEP 9

RESULT 6
US-09-956-206A-21
; Sequence 21, Application US/09956206A
; Patent No. US20020164339A1
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO I.
; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; M33 ANTI-B46 ANTIBODY, METHODS OF USE THEREOF, AND
; METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER

```

STREET: 755 Page Mill Road  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304-1018  
 COMPUTER: PEADARLE FORM  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1 0, Version #1 30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/466,206A  
 FILING DATE: 19-Apr-2002  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/525,530  
 FILING DATE: 14-SEP-1995  
 APPLICATION NUMBER: PCT/US95/11693  
 FILING DATE: 14 SEP-1995  
 APPLICATION NUMBER: 08/487,508  
 FILING DATE: 7-JUNE-1995  
 APPLICATION NUMBER: 08/307,968  
 FILING DATE: 16-SEPT-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: WITT, ERIC  
 REGISTRATION NUMBER: 44,408  
 REFERENCE/DOC#ET NUMBER: 276330000101  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 813-5600  
 TELEFAX: (650) 494-0792  
 TELEX: 706141

INFORMATION FOR SEQ ID NO. 21:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 26 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO. 21:  
 US 09-056-206A-21

Query Match 100.0%; Score 20; DB 0; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 83;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4  
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 Db 1 VLEP 4

RESULT 7  
 US-09-864-761-36931  
 ; Sequence 36931, Application US/09864761  
 ; Patent No. US20020048761A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharon G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Wensheng  
 ; TITLE OF INVENTION: HUMAN GENOME-DEPENDED SINGLE EXON NUCLEOTIC ACID PROBES USEFUL FOR  
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
 ; FILE REFERENCE: Aecmca-X-1  
 ; CURRENT APPLICATION NUMBER: US/09/864,761  
 ; CURRENT FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/180,332  
 ; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/632,366  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: GB 24263-6  
 ; PRIOR FILING DATE: 2000-10-04  
 ; PRIOR APPLICATION NUMBER: US 60/236,359  
 ; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: US 60/234,687  
 ; PRIOR FILING DATE: 2000-09-21  
 ; PRIOR APPLICATION NUMBER: US 09/608,408  
 ; PRIOR FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: US 09/774,203  
 ; PRIOR FILING DATE: 2001-01-29  
 ; NUMBER OF SEQ ID NOS: 49117  
 ; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
 ; SEQ ID NO 36931  
 ; LENGTH: 27  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: MAP TO A0007740.1  
 ; OTHER INFORMATION: EXPRESSED IN HELL100, SIGNAL = 1  
 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.94  
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.98  
 ; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.59  
 ; OTHER INFORMATION: EXPRESSED IN EPAIN, SIGNAL = 0.74  
 ; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.83  
 ; OTHER INFORMATION: EXPRESSED IN PT474, SIGNAL = 1.2  
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.8  
 ; OTHER INFORMATION: EXPRESSED IN ACULT LIVER, SIGNAL = 0.77  
 ; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9e+02  
 ; US-09-864-761-36931

Query Match 100.0%; Score 20; DB 10; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 87;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4  
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 Db 20 VLEP 23

RESULT 8  
 US-09-920-552-45  
 ; Sequence 45, Application US/09920552  
 ; Patent No. US20020094576A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Griffiths, David J.  
 ; APPLICANT: Weiss, Robin A.  
 ; APPLICANT: Venables, Patrick  
 ; TITLE OF INVENTION: Material  
 ; FILE REFERENCE: Abbott Labs  
 ; CURRENT APPLICATION NUMBER: US/09/320,553  
 ; CURRENT FILING DATE: 2001-08-01  
 ; PRIOR APPLICATION NUMBER: 09/299,329  
 ; PRIOR FILING DATE: 1999-03-29  
 ; PRIOR APPLICATION NUMBER: GB 0906649.1  
 ; PRIOR FILING DATE: 1998-03-27  
 ; PRIOR APPLICATION NUMBER: 00/115,288  
 ; PRIOR FILING DATE: 1999-01-08

NUMBER OF SEQ ID NOS: 127  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 45  
LENGTH: 28  
TYPE: PRT  
ORGANISM: Rous sarcoma virus  
US-09 920 592-45

Query Match 100.0%, Score 20, DB 10, Length 29,  
Best Local Similarity 100.0%, Pred No 1, 20, 02,  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

QY 1 VLEP 4  
Db 22 VLEP 25

RESULT 9  
US-09-864-761-41269  
Sequence 41269, Application US/09864761  
Patent No US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENE DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
FILE REFERENCE: Aecmca X-1  
CURRENT APPLICATION NUMBER: US 09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/237,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US 1/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/509,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Ammax Sequence Listing Engine vers 1.1  
SEQ ID NO 41269  
LENGTH: 37  
TYPE: PRT  
ORGANISM: Homo sapiens

FEATURE:  
OTHER INFORMATION: MAP TO AL133295.11  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7  
OTHER INFORMATION: PBT HUMAN HIT: AW630487.1, EVALUATE 1 00e-15  
US-09-864-761-41269

Query Match 100.0%, Score 20, DB 10, Length 37,  
Best Local Similarity 100.0%, Pred No 1, 20, 02,  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

QY 1 VLEP 4  
Db 33 VLEP 36

RESULT 10  
US-09-864-761-35818  
Sequence 35818, Application US/09864761  
Patent No US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENE DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
FILE REFERENCE: Aecmca X-1  
CURRENT APPLICATION NUMBER: US 09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/237,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/630,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/336,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
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PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/509,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Ammax Sequence Listing Engine vers 1.1

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? SEQ ID NO 35818
? LENGTH: 42
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: MAP TO AC009308.3
? OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL - 2
? OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL - 1.6
? OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL - 1.8
? OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL - 1.4
? OTHER INFORMATION: EXPRESSED IN HEPT, SIGNAL - 1.9
? OTHER INFORMATION: EXPRESSED IN HPAIN, SIGNAL - 2
? OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
? OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1
? OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL - 2
? OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL - 1.6
? OTHER INFORMATION: EST HUMAN HIT: A1308220.1, EVALUATE 3.60e+00
? OTHER INFORMATION: SWISSPROT HIT: P17565, EVALUATE 3.60e+00
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US-09-864-761-35818

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Query March 100.0%, Score 20, PP 10, Length 42,
Best Local Similarity 100.0%, Pred. No. 1.4e+02,
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0,
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OY 1 VLEP 4
    ||||
DB 24 VLEP 27
```

RESULT 11

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US-09-925-299-784
? Sequence 784, Application US/09925299
? Publication No. US20030040617A9
? GENERAL INFORMATION:
? APPLICANT: Posen et al.
? TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
? FILE REFERENCE: PA102
? CURRENT APPLICATION NUMBER: US/09/025,299
? PRIOR FILING DATE: 2001-08-10
? PRIOR APPLICATION NUMBER: PCT/US00/05883
? PRIOR FILING DATE: 2000-03-08
? PRIOR APPLICATION NUMBER: 60/124,270
? PRIOR FILING DATE: 1999-03-12
? NUMBER OF SEQ ID NOS: 1556
? SOFTWARE: Patent In Ver. 2.0
? SEQ ID NO 784
? LENGTH: 44
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-09-925-299-784
```

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Query March 100.0%, Score 20, PP 9, Length 44;
Best Local Similarity 100.0%, Pred. No. 1.5e+02;
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
```

```
OY 1 VLEP 4
    ||||
DB 19 VLEP 22
```

RESULT 12

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US-09-925-299-784
? Sequence 784, Application US/09925299
? Publication No. US20030040617A1
? GENERAL INFORMATION:
? APPLICANT: Posen et al.
? TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
? FILE REFERENCE: PA102
? CURRENT APPLICATION NUMBER: US/09/025,299
? PRIOR FILING DATE: 2001-08-10
? PRIOR APPLICATION NUMBER: PCT/US00/05883
? PRIOR FILING DATE: 2000-03-08
? PRIOR APPLICATION NUMBER: 60/124,270
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? PRIOR FILING DATE: 1999-03-12
? NUMBER OF SEQ ID NOS: 1556
? SOFTWARE: Patent In Ver. 2.0
? SEQ ID NO 784
? LENGTH: 44
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-09-925-299-784
```

```
Query March 100.0%, Score 20, PP 10, Length 44;
Best Local Similarity 100.0%, Pred. No. 1.5e+02;
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
```

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OY 1 VLEP 4
    ||||
DB 19 VLEP 22
```

RESULT 13

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US-09-864-761-46702
? Sequence 46702, Application US/09864761
? Patent No. US20030040763A1
? GENERAL INFORMATION:
? APPLICANT: Penn, Sharron G.
? APPLICANT: Rank, David R.
? APPLICANT: Hanzel, David K.
? APPLICANT: Chen, Wensheng
? TITLE OF INVENTION: HUMAN GENE DERIVED SINGLE EXON NUCLEOTIC ACID IN RED BLOOD CELL
? TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
? FILE REFERENCE: Aomic-X-1
? CURRENT APPLICATION NUMBER: US/09/864,761
? PRIOR FILING DATE: 2001-09-23
? PRIOR APPLICATION NUMBER: US 60/180,312
? PRIOR FILING DATE: 2000-02-04
? PRIOR APPLICATION NUMBER: US 60/207,456
? PRIOR FILING DATE: 2000-05-26
? PRIOR APPLICATION NUMBER: US 60/632,166
? PRIOR FILING DATE: 2000-08-03
? PRIOR APPLICATION NUMBER: GP 24263.6
? PRIOR FILING DATE: 2000-10-04
? PRIOR APPLICATION NUMBER: US 60/236,359
? PRIOR FILING DATE: 2000-09-27
? PRIOR APPLICATION NUMBER: PCT/US01/00666
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00667
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00664
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00669
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00665
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00668
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00663
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00662
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00661
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00670
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: US 60/234,687
? PRIOR FILING DATE: 2000-09-21
? PRIOR APPLICATION NUMBER: US 60/604,408
? PRIOR FILING DATE: 2000-06-30
? PRIOR APPLICATION NUMBER: US 60/774,203
? PRIOR FILING DATE: 2001-01-29
? NUMBER OF SEQ ID NOS: 49117
? SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
? SEQ ID NO 46702
? LENGTH: 47
? TYPE: PRT
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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AF064863.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.91
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
; OTHER INFORMATION: SWISSPROT HIT: Q10443, EVALUATE 0.00+0.00
US 09 864 761-46702

Query Match 100.0%; Score 20; PB 10; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 7 VLEP 10

RESULT 14
US-09-205-658-174
; Sequence 174, Application US/09205658
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Ravkum, Gary
; TITLE OF INVENTION: THERAPEUTIC ARE DIAGNOSTIC TOOLS FOR
; FILE REFERENCE: 00986/351004
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 174
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Mus musculus or Homo sapiens or C elegans
US-09-205-658-174

Query Match 100.0%; Score 20; PB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 26 VLEP 20

RESULT 15
US 09 864 761-40223
; Sequence 40223, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME DERIVED SINGLE EXON NUCLEOTIDE AND PROBES USEFUL FOR
; FILE REFERENCE: Accmiga X 1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26

```

```

; PRIOR APPLICATION NUMBER: US 09/632,766
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-10
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 40223
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011111.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EST_HUMAN HIT: EF55535.1, EVALUATE 0.00e-01
US 09 864 761-40223

Query Match 100.0%; Score 20; PB 10; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 18 VLEP 21

RESULT 16
US-09-864-761-37977
; Sequence 37977, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME DERIVED SINGLE EXON NUCLEOTIDE AND PROBES USEFUL FOR
; FILE REFERENCE: Accmiga X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23

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1 PRIOR APPLICATION NUMBER: US 69/180,312
2 PRIOR FILING DATE: 2000-02-04
3 PRIOR APPLICATION NUMBER: US 69/207,456
4 PRIOR FILING DATE: 2000-05-26
5 PRIOR APPLICATION NUMBER: US 69/632,366
6 PRIOR FILING DATE: 2000-08-03
7 PRIOR APPLICATION NUMBER: GR 24263.6
8 PRIOR FILING DATE: 2000-10-04
9 PRIOR APPLICATION NUMBER: US 69/236,359
10 PRIOR FILING DATE: 2000-09-27
11 PRIOR APPLICATION NUMBER: PCT/US01/00666
12 PRIOR FILING DATE: 2001-01-30
13 PRIOR APPLICATION NUMBER: PCT/US01/00667
14 PRIOR FILING DATE: 2001-01-30
15 PRIOR APPLICATION NUMBER: PCT/US01/00664
16 PRIOR FILING DATE: 2001-01-30
17 PRIOR APPLICATION NUMBER: PCT/US01/00664
18 PRIOR FILING DATE: 2001-01-30
19 PRIOR APPLICATION NUMBER: PCT/US01/00665
20 PRIOR FILING DATE: 2001-01-30
21 PRIOR APPLICATION NUMBER: PCT/US01/00668
22 PRIOR FILING DATE: 2001-01-30
23 PRIOR APPLICATION NUMBER: PCT/US01/00663
24 PRIOR FILING DATE: 2001-01-30
25 PRIOR APPLICATION NUMBER: PCT/US01/00662
26 PRIOR FILING DATE: 2001-01-30
27 PRIOR APPLICATION NUMBER: PCT/US01/00661
28 PRIOR FILING DATE: 2000-06-30
29 PRIOR APPLICATION NUMBER: US 69/608,408
30 PRIOR FILING DATE: 2000-06-30
31 PRIOR APPLICATION NUMBER: US 69/774,203
32 PRIOR FILING DATE: 2001-01-29
33 NUMBER OF SEQ ID NOS: 49117
34 SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
35 SEQ ID NO 37877
36 LENGTH: 52
37 TYPE: PRT
38 ORGANISM: Homo sapiens
39 FEATURE:
40 OTHER INFORMATION: MAP TO AC012140.1
41 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.96
42 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
43 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.96
44 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
45 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.99
46 OTHER INFORMATION: EXPRESSED IN HEPT, SIGNAL = 1.1
47 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
48 OTHER INFORMATION: SWISSPOT HIT: C75031, EVALUATION 0.00602
US-09-864-761-44895

Query Match 100.0%; Score 20; DB 10; Length 52;
Best Local Similarity 100.0%; Pred No 1 de.02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 9 VLEP 12

RESULT 17
US-09-864-761-44895
; Sequence 44895, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David P.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENE DERIVED SINGLE EXON NUCLEOTIC ACID SEQUENCES USEFUL FOR

```

```

1 TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
2 FILE REFERENCE: Aomic X-1
3 CURRENT APPLICATION NUMBER: US 69/864,761
4 CURRENT FILING DATE: 2001-05-23
5 PRIOR APPLICATION NUMBER: US 69/180,312
6 PRIOR FILING DATE: 2000-02-04
7 PRIOR APPLICATION NUMBER: US 69/207,456
8 PRIOR FILING DATE: 2000-05-26
9 PRIOR APPLICATION NUMBER: US 69/632,366
10 PRIOR FILING DATE: 2000-08-03
11 PRIOR APPLICATION NUMBER: GR 24263.6
12 PRIOR FILING DATE: 2000-10-04
13 PRIOR APPLICATION NUMBER: US 69/236,359
14 PRIOR FILING DATE: 2000-09-27
15 PRIOR APPLICATION NUMBER: PCT/US01/00666
16 PRIOR FILING DATE: 2001-01-30
17 PRIOR APPLICATION NUMBER: PCT/US01/00667
18 PRIOR FILING DATE: 2001-01-30
19 PRIOR APPLICATION NUMBER: PCT/US01/00664
20 PRIOR FILING DATE: 2001-01-30
21 PRIOR APPLICATION NUMBER: PCT/US01/00664
22 PRIOR FILING DATE: 2001-01-30
23 PRIOR APPLICATION NUMBER: PCT/US01/00665
24 PRIOR FILING DATE: 2001-01-30
25 PRIOR APPLICATION NUMBER: PCT/US01/00668
26 PRIOR FILING DATE: 2001-01-30
27 PRIOR APPLICATION NUMBER: PCT/US01/00663
28 PRIOR FILING DATE: 2001-01-30
29 PRIOR APPLICATION NUMBER: PCT/US01/00662
30 PRIOR FILING DATE: 2001-01-30
31 PRIOR APPLICATION NUMBER: PCT/US01/00661
32 PRIOR FILING DATE: 2000-06-30
33 PRIOR APPLICATION NUMBER: US 69/608,408
34 PRIOR FILING DATE: 2000-06-30
35 PRIOR APPLICATION NUMBER: US 69/774,203
36 PRIOR FILING DATE: 2001-01-29
37 NUMBER OF SEQ ID NOS: 49117
38 SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
39 SEQ ID NO 44895
40 LENGTH: 53
41 TYPE: PRT
42 ORGANISM: Homo sapiens
43 FEATURE:
44 OTHER INFORMATION: MAP TO AC019194.2
45 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.48
46 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
47 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.78
48 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.74
49 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
50 OTHER INFORMATION: EST HUMAN HIT: A4898971, EVALUATION 0.00625
51 OTHER INFORMATION: SWISSPOT HIT: P77640, EVALUATION 0.00602
US-09-864-761-44895

Query Match 100.0%; Score 20; DB 10; Length 53;
Best Local Similarity 100.0%; Pred No 1 de.02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 31 VLEP 34

RESULT 18
US-09-925-300-1385
; Sequence 1385, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Eden

```

```

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/99/025,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 69/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.1.0
; SEQ ID NO 1385
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 159
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-500-1385

Query Match: 100.0%, Score 20, DB 10, Length 56;
Best Local Similarity 100.0%, Freq. No. 1.9e+02,
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

QY 1 VLEP 4
DB 30 VLEP 33
|||||

RESULT 19
US-09-864-761-34003
; Sequence 34003, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBE USEFUL FOR
; TITLE OF INVENTION: SHRNA EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecm1Ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 69/832,566
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30

```

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; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34003
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006017.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.85
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BONE MAPPW, SIGNAL = 0.85
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.96
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.91
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BPAIN, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.93
; OTHER INFORMATION: EST HUMAN HIT: AW270405.1, FVALUE 8.00e-20
; OTHER INFORMATION: SWISSPROT HIT: Q0U1F2, FVALUE 4.40e+00
US-09-864-761-34003

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```

Query Match: 100.0%, Score 20, DB 10, Length 61;
Best Local Similarity 100.0%, Freq. No. 2.1e+02;
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

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QY 1 VLEP 4
DB 29 VLEP 32
|||||

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```

RESULT 20
US-09-864-761-43009
; Sequence 43009, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBE USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecm1Ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 69/832,566
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GR 24203.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00671
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00672
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00673
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00674
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00675
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00676
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00677
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00678
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00679
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00680
; PRIOR FILING DATE: 2001-01-30

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1 PRIOR APPLICATION NUMBER: PCT/US01/00663  
2 PRIOR FILING DATE: 2001-01-30  
3 PRIOR APPLICATION NUMBER: PCT/US01/00662  
4 PRIOR FILING DATE: 2001-01-30  
5 PRIOR APPLICATION NUMBER: PCT/US01/00661  
6 PRIOR FILING DATE: 2001-01-30  
7 PRIOR APPLICATION NUMBER: PCT/US01/00670  
8 PRIOR FILING DATE: 2001-01-30  
9 PRIOR APPLICATION NUMBER: US 60/234,687  
10 PRIOR FILING DATE: 2000-09-21  
11 PRIOR APPLICATION NUMBER: US 09/608,408  
12 PRIOR FILING DATE: 2000-04-13  
13 PRIOR APPLICATION NUMBER: US 09/774,203  
14 PRIOR FILING DATE: 2001-01-29  
15 NUMBER OF SEQ ID NOS: 49117  
16 SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
17 SEQ ID NO 43309  
18 LENGTH: 63  
19 TYPE: PRT  
20 ORGANISM: Homo sapiens  
21 FEATURE:  
22 OTHER INFORMATION: MAP TO AC004108.1  
23 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.71  
24 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.61  
25 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.75  
26 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.73  
27 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.65  
28 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.78  
29 OTHER INFORMATION: SWISSPROT HIT: P32595, EVALUATION: 6.80e-01  
30 OTHER INFORMATION: PCT\_HUMAN HIT: P67516, EVALUATION: 9.70e-01  
31 US-09-864 761-43309

Query Match 100.0% Score 20; DR 10; Length 63;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4

DB 23 VLEP 26

RESULT 21  
US-09-864-761-43309  
1 Sequence 17, Application US/09/0908011A  
2 Patent No. US2002004892A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Inouye, Sumiko  
5 APPLICANT: Hsu, Wei-Yin  
6 APPLICANT: Eagle, Susan  
7 APPLICANT: Inouye, Masayori  
8 TITLE OF INVENTION: POLYADENYLIC PEPPER TRANSSCRIPTASE  
9 NUMBER OF SEQUENCES: 52  
10 CORRESPONDENCE ADDRESS:  
11 ADDRESSEE: WEISER & ASSOCIATES  
12 STREET: 230 South Fifteenth Street, Suite 500  
13 CITY: Philadelphia  
14 STATE: PA  
15 COUNTRY: USA  
16 ZIP: 19102  
17 COMPUTER READABLE FORM:  
18 MEDIUM TYPE: Floppy disk  
19 COMPUTER: IBM PC compatible  
20 OPERATING SYSTEM: WINDOWS DOS  
21 SOFTWARE: Patent in Release #1.0, Version #1.0  
22 CURRENT APPLICATION DATA:  
23 APPLICATION NUMBER: US/09/0908011A  
24 FILING DATE: 03-MAR-1997  
25 CLASSIFICATION: 435  
26 ATTORNEY/AGENT INFORMATION:  
27 NAME: Weiser, Gerard J.  
28 REGISTRATION NUMBER: 19,763  
29 REFERENCE/DOC# NUMBER: 377(913).5889P  
30 TELECOMMUNICATION INFORMATION:

1 TELEPHONE: 215-875-8383  
2 TELEFAX: 215-875-8394  
3 INFORMATION FOR SEQ ID NO: 17:  
4 SEQUENCE CHARACTERISTICS:  
5 LENGTH: 65 amino acids  
6 TYPE: amino acid  
7 STRANDEDNESS:  
8 TOPOLOGY: linear  
9 MOLECULE TYPE: protein  
10 US-08-808-031A-17

Query Match 100.0% Score 20; DR 8; Length 65;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4

DB 24 VLEP 27

RESULT 22  
US-09-864-761-39828  
1 Sequence 39828, Application US/090864761  
2 Patent No. US20020048763A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Penn, Sharron G.  
5 APPLICANT: Park, David P.  
6 APPLICANT: Hanzel, David K.  
7 APPLICANT: Chen, Wensheng  
8 TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
9 FILE REFERENCE: Aomic-X-1  
10 CURRENT APPLICATION NUMBER: US/09/090864, 761  
11 PRIOR FILING DATE: 2001-05-23  
12 PRIOR APPLICATION NUMBER: US 60/180,312  
13 PRIOR FILING DATE: 2000-02-04  
14 PRIOR APPLICATION NUMBER: US 60/207,456  
15 PRIOR FILING DATE: 2000-05-26  
16 PRIOR APPLICATION NUMBER: US 09/632,166  
17 PRIOR FILING DATE: 2000-08-03  
18 PRIOR APPLICATION NUMBER: GB 24263.6  
19 PRIOR FILING DATE: 2000-10-04  
20 PRIOR APPLICATION NUMBER: US 60/236,159  
21 PRIOR FILING DATE: 2000-09-27  
22 PRIOR APPLICATION NUMBER: PCT/US01/00666  
23 PRIOR FILING DATE: 2001-01-30  
24 PRIOR APPLICATION NUMBER: PCT/US01/00667  
25 PRIOR FILING DATE: 2001-01-30  
26 PRIOR APPLICATION NUMBER: PCT/US01/00664  
27 PRIOR FILING DATE: 2001-01-30  
28 PRIOR APPLICATION NUMBER: PCT/US01/00669  
29 PRIOR FILING DATE: 2001-01-30  
30 PRIOR APPLICATION NUMBER: PCT/US01/00665  
31 PRIOR FILING DATE: 2001-01-30  
32 PRIOR APPLICATION NUMBER: PCT/US01/00668  
33 PRIOR FILING DATE: 2001-01-30  
34 PRIOR APPLICATION NUMBER: PCT/US01/00663  
35 PRIOR FILING DATE: 2001-01-30  
36 PRIOR APPLICATION NUMBER: PCT/US01/00662  
37 PRIOR APPLICATION NUMBER: PCT/US01/00661  
38 PRIOR FILING DATE: 2001-01-30  
39 PRIOR APPLICATION NUMBER: PCT/US01/00670  
40 PRIOR FILING DATE: 2001-01-30  
41 PRIOR APPLICATION NUMBER: US 60/234,687  
42 PRIOR FILING DATE: 2000-09-21  
43 PRIOR APPLICATION NUMBER: US 09/608,408  
44 PRIOR FILING DATE: 2000-06-30  
45 PRIOR APPLICATION NUMBER: US 09/774,203  
46 PRIOR FILING DATE: 2001-01-29  
47 NUMBER OF SEQ ID NOS: 49117  
48 SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
49 SEQ ID NO 39828

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; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO ACC05939.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.0
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.8
; OTHER INFORMATION: EST HUMAN HIT: BP038034, EVALUATE 1.00e 01
; OTHER INFORMATION: SWISSPROT HIT: Q14514, EVALUATE 3.00e 00
US-09-864-761-39829

Query Match: 100.0%, Score 20, DB 10, Length 65,
Best Local Similarity: 100.0%, Ref: No. 2, 3e+02,
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 VLEP 4
DB 36 VLEP 39

RESULT 23
US-09-864-761-42067
; Sequence 42067, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G
; APPLICANT: Park, David B
; APPLICANT: Hanzel, David K
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID SEQUENCE REFIL FOR
; FILE REFERENCE: Aecmca X 1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/242,616
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30

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; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 42067
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL049780.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EST HUMAN HIT: AW500159, EVALUATE 5.00e-35
; OTHER INFORMATION: SWISSPROT HIT: P21800, EVALUATE 1.00e-04
US-09-864-761-42067

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Query Match: 100.0%, Score 20, DB 10, Length 66;
Best Local Similarity: 100.0%, Ref: No. 3, 3e+02;
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

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QY 1 VLEP 4
DB 25 VLEP 28

RESULT 24
US-09-864-761-48913
; Sequence 48913, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G
; APPLICANT: Park, David B
; APPLICANT: Hanzel, David K
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID SEQUENCE REFIL FOR
; FILE REFERENCE: Aecmca X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/242,616
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-10
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-20
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers 1.1
; SEQ ID NO 48913
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL121716.2
; OTHER INFORMATION: EXPRESSED IN R1474, SIGNAL = 1
; OTHER INFORMATION: SWISSEPT HIT: CgY3P6, EVALUE 1.00e-03
; OTHER INFORMATION: EST_HUMAN HIT: AK625526.1, EVALUE 3.00e-10
US-09-864-761-48913

Query Match 100.0%; Score 20; DP 10; Length 67;
Best Local Similarity 100.0%; Pred N=2, I=0, Gaps 0,
Matches 4; Conservative 0; Mismatches 0; Indels 0, Gaps 0,

QY 1 VLEP 4
Db 15 VLEP 18

RESULT 25
US-09-925-301-1660
; Sequence 1660, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1660
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (9)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (12)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (20)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (21)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (24)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (25)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (29)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE

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; LOCATION: (39)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (45)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (51)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (52)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (66)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1660

Query Match 100.0%; Score 20; DP 10; Length 68;
Best Local Similarity 100.0%; Pred N=2, I=0, Gaps 0,
Matches 4; Conservative 0; Mismatches 0; Indels 0, Gaps 0,

QY 1 VLEP 4
Db 56 VLEP 59

Search completed: March 5, 2003, 08:37:51
Job time : 14 secs

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GenCore version 5.1.3  
Copyright (c) 1993 2003 Compugen Ltd

OM protein - protein search, using sw mod-1

Run on: Match 5, 2003, 08:11:35, Search time 14 seconds  
(without alignments)  
8,407 Million cell updates/sec

Title: US-09-732-411-15

Perfect score: 20

Sequence: 1 VLEP 4

Scoring table: BLASTW62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 28422222 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database:

Issued Patents AA.\*

1: /cgn2\_6/prodata/1/1aa/6A COMB pep.\*

2: /cgn2\_6/prodata/1/1aa/6B COMB pep.\*

3: /cgn2\_6/prodata/1/1aa/6A COMB pep.\*

4: /cgn2\_6/prodata/1/1aa/6B COMB pep.\*

5: /cgn2\_6/prodata/1/1aa/6C COMB pep.\*

6: /cgn2\_6/prodata/1/1aa/6D COMB pep.\*

Pref No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	9	4	US-08-737-109-5
2	20	100.0	19	4	US-08-928-213R-35
3	20	100.0	19	4	US-08-001-944C-72
4	20	100.0	25	1	US-08-127-803-20
5	20	100.0	25	2	US-08-453-353-20
6	20	100.0	25	3	US-08-011-555-5
7	20	100.0	26	1	US-07-942-345-281
8	20	100.0	26	4	US-08-526-639A-21
9	20	100.0	34	2	US-08-067-504-1
10	20	100.0	34	3	US-08-067-504-1
11	20	100.0	34	5	PCT US94-02552-1
12	20	100.0	35	4	US-08-082-279P-504
13	20	100.0	35	4	US-08-315-104B-504
14	20	100.0	40	4	US-08-314-264-106
15	20	100.0	65	6	4320058.17
16	20	100.0	70	4	US-08-134-001C-4579
17	20	100.0	75	4	US-08-028-183R-13
18	20	100.0	82	4	US-08-655-270A-25
19	20	100.0	93	3	US-09-208-804-3
20	20	100.0	93	3	US-08-801-743-3
21	20	100.0	98	3	US-08-478-097A-5
22	20	100.0	100	2	US-08-963-601-2
23	20	100.0	105	3	US-08-484-551R-619
24	20	100.0	108	3	US-08-388-353-639
25	20	100.0	112	3	US-08-027-413-7
26	20	100.0	114	1	US-08-481-377-27
27	20	100.0	114	2	US-08-491-846-25

28	20	100.0	114	3	US-09-153-733A-27
29	20	100.0	114	3	US-08-946-002A-25
30	20	100.0	114	4	US-08-172-662-25
31	20	100.0	114	4	US-09-301-520D-25
32	20	100.0	114	4	US-08-389-705-27
33	20	100.0	114	5	PCT US94-02552-1
34	20	100.0	114	5	PCT US94-00685-25
35	20	100.0	120	4	US-08-485-953-2
36	20	100.0	126	4	US-04-114-001C-5404
37	20	100.0	126	4	US-08-935-223-306
38	20	100.0	126	4	US-08-433-248A-8
39	20	100.0	130	1	US-08-426-627-18
40	20	100.0	139	4	US-08-367-953B-114
41	20	100.0	139	4	US-08-367-953B-118
42	20	100.0	139	4	US-08-367-953B-131
43	20	100.0	143	3	US-08-725-459B-43
44	20	100.0	156	3	US-08-826-246-10
45	20	100.0	156	3	US-08-944-496-10
46	20	100.0	156	3	US-08-126-640-11
47	20	100.0	156	4	US-08-925-588-10
48	20	100.0	156	4	US-08-388-292A-33
49	20	100.0	160	4	US-08-247-155-156
50	20	100.0	161	3	US-08-346-164-2

## ALIGNMENTS

### RESULT 1

US-08-737-109-5

Sequence 5, Application US/08/37109

Patent No. 6455688

GENERAL INFORMATION:

APPLICANT: SLARAS, Antoni Pyszard

APPLICANT: ELBOPOUCH, Kieran Michael

APPLICANT: BRIGHT, Simon William Jonathan

APPLICANT: PENTEM, Philip Anthony

TITLE OF INVENTION: Plant Gene Specifying Acetyl Coenzyme A

TITLE OF INVENTION: Carboxylase and Transformed Plants Containing Same

NUMBER OF SEQUENCES: 32

CORRESPONDENT ADDRESS:

ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.

STREET: 1100 New York Avenue, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette

COMPUTER: IBM PC compatible

OPERATING SYSTEM: P-PC2/MS-DOS

SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/737,109

FILING DATE: 21-OCT-1996

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB94/50846

FILING DATE: 02-MAY-1994

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

ORGANISM: Avena sativa

US-08-737-109-5

Query Match 100.0%, Score 20, DB 4, Length 9;

Best Local Similarity 100.0%, Pred No. 1.9e-05;

Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VLEP 4  
1111  
DB 2 VLEP 5

## RESULT 2

US-08-928-213B-35  
; Sequence 35, Application US/09001984C  
; Patent No. 6245331  
; GENERAL INFORMATION:  
; APPLICANT: McHenry, Charles S.  
; ; Seville, Mark  
; ; Cull, Millard G.  
; TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III  
; ; HOMOZYME  
; NUMBER OF SEQUENCES: 195  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 200 Montgomery Street, Suite 2000  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/928,213B  
FILING DATE: 12-Sep-1997  
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/POWET NUMBER: ENZYCO-02550  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-705 8410  
TELEFAX: 415-397-8338

INFORMATION FOR SEQ ID NO. 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO. 35:

US-08-928 213B 35

Query Match 100.0%; Score 20; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred No. 72;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4  
1111  
DB 1 VLEP 4

## RESULT 3

US-09-001-984C-72  
; Sequence 72, Application US/09001984C  
; Patent No. 6245331  
; GENERAL INFORMATION:  
; APPLICANT: Laal, Suman  
; APPLICANT: Zolla-Pazner, Susan  
; APPLICANT: Belisle, John T.  
; TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE  
; FILE REFERENCE: NYU-011  
; CURRENT APPLICATION NUMBER: US/09/001,984C  
; CURRENT FILING DATE: 1997-12-31  
; PRIOR APPLICATION NUMBER: 63/034,003  
; PRIOR FILING DATE: 1996-12-31

; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 72  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Mycobacterium tuberculosis strain H37Pv  
US-09-001-984C-72

Query Match 100.0%; Score 20; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred No. 72;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4  
1111  
DB 15 VLEP 18

## RESULT 4

US-08-127-909-20  
; Sequence 20, Application US/08127909  
; Patent No. 5436528  
; GENERAL INFORMATION:  
; APPLICANT: Postlethwaite, Arnold E.  
; APPLICANT: Seyer, Jerome  
; APPLICANT: Kang, Andrew  
; TITLE OF INVENTION: CHEMOTACTIC WOUND HEALING PEPTIDES  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 11530

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08127,909  
FILING DATE:

CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 90202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 210 901 SANS UR  
INFORMATION FOR SEQ ID NO. 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-127-909-20

Query Match 100.0%; Score 20; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred No. 95;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4  
1111  
DB 4 VLEP 7

## RESULT 5

US-08-457-353-20  
; Sequence 20, Application US/08457353  
; Patent No. 5824647  
; GENERAL INFORMATION:

```

; APPLICANT: Postlethwaite, Arnold E.
; APPLICANT: Seyer, Jerome
; APPLICANT: Kang, Andrew
; TITLE OF INVENTION: CHEMOTACTIC WOUND HEALING PEPTIDES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.05
; CURRENT APPLICATION NUMBER: US/98/457,353
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,146
; REFERENCE/DOCET NUMBER: 9202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO. 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US 09 457-353-20

```

```

Query Match 100.0%; Score 20; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 VLEP 4
Db 4 VLEP 7

```

```

RESULT 6
US-09-011-525-5
; Sequence 5, Application US/99011525
; Patent No. 6020172
; GENERAL INFORMATION:
; APPLICANT: BOTH, GERALD W.
; TITLE OF INVENTION: GENE THERAPY USING OVINE ADENOVIRAL VECTORS
; FILE REFERENCE: Gene Therapy Using Ovine Adenoviral Ve
; CURRENT APPLICATION NUMBER: US/99/011,525
; CURRENT FILING DATE: 1998-04-20
; EARLIER APPLICATION NUMBER: PCT/AUSK/980519
; EARLIER FILING DATE: 1996-08-14
; EARLIER APPLICATION NUMBER: AU PN4776
; EARLIER FILING DATE: 1995-08-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Ovine adenovirus
US-09-011-525-5

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Query Match 100.0%; Score 20; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VLEP 4

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```

Db 7 VLEP 10
RESULT 7
US-07-942-245-281
; Sequence 281, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: ROOS, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE PEPTIDE VARIANTS OF RECOMB
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughraue, Michl, Zirm, Marjorie & Ceas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09 SEP.1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO. 281:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-942-245-281

```

```

Query Match 100.0%; Score 20; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 1 VLEP 4
Db 5 VLEP 8

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```

RESULT 8
US-08-525-539A-21
; Sequence 21, Application US/0805539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: BOGUTTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.
; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: M33 ANTI-BAG6 ANTIBODY, METHODS OF USE THEREOF, AND
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & MORRISON
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 434
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/POCKET NUMBER: 37,612
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO. 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-525-539A 21

Query Match 100.0%, Score 20, DB 4, Length 26,
Best Local Similarity 100.0%, Pred. No. 1.3e+02,
Matches 4, Conservative 0, Mismatches 0, Indels 0; Gaps 0;

QY 1 VLEP 4
DB 1 VLEP 4

; INFORMATION FOR SEQ ID NO. 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-525-539A 21

Query Match 100.0%, Score 20, DB 4, Length 26,
Best Local Similarity 100.0%, Pred. No. 1.3e+02,
Matches 4, Conservative 0, Mismatches 0, Indels 0; Gaps 0;

QY 1 VLEP 4
DB 1 VLEP 4

; INFORMATION FOR SEQ ID NO. 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-525-539A 21

```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-967-508-1

Query Match 100.0%, Score 20, DB 2, Length 34,
Best Local Similarity 100.0%, Pred. No. 1.3e+02,
Matches 4, Conservative 0, Mismatches 0, Indels 0; Gaps 0;

QY 1 VLEP 4
DB 7 VLEP 10

; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-967-506-1

Query Match 100.0%, Score 20, DB 3, Length 34,
Best Local Similarity 100.0%, Pred. No. 1.3e+02,
Matches 4, Conservative 0, Mismatches 0, Indels 0; Gaps 0;

QY 1 VLEP 4
DB 7 VLEP 10

; INFORMATION FOR SEQ ID NO. 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-967-506-1

Query Match 100.0%, Score 20, DB 3, Length 34,
Best Local Similarity 100.0%, Pred. No. 1.3e+02,
Matches 4, Conservative 0, Mismatches 0, Indels 0; Gaps 0;

QY 1 VLEP 4
DB 7 VLEP 10

```

```

; INFORMATION FOR SEQ ID NO. 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-967-506-1

Query Match 100.0%, Score 20, DB 3, Length 34,
Best Local Similarity 100.0%, Pred. No. 1.3e+02,
Matches 4, Conservative 0, Mismatches 0, Indels 0; Gaps 0;

QY 1 VLEP 4
DB 7 VLEP 10

; INFORMATION FOR SEQ ID NO. 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-967-506-1

Query Match 100.0%, Score 20, DB 3, Length 34,
Best Local Similarity 100.0%, Pred. No. 1.3e+02,
Matches 4, Conservative 0, Mismatches 0, Indels 0; Gaps 0;

QY 1 VLEP 4
DB 7 VLEP 10

```



```

RESULT 11.
PCT-US94-02552-1
; Sequence 1, Application PC/TUS9402552
; GENERAL INFORMATION:
; APPLICANT: Elhammer, Ale P
; APPLICANT: Homa, Fred L
; TITLE OF INVENTION: A cloned cDNA encoding a UDP GalNA-
; TITLE OF INVENTION: Polypeptide, N-Acetylgalactosaminyltransferase
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Upjohn Company, Corp. Intellectual
; ADDRESSEE: Property Law
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: Michigan
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM.
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1 0, Version #1 25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02552
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Darneley Jr., James D.
; REGISTRATION NUMBER: 33,673
; REFERENCE/BOOK NUMBER: 4755 P 7P
; TELECOMMUNICATION INFORMATION
; TELEPHONE: 616-385-5210
; TELEFAX: 616-385-6897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO. 1.
; SEQUENCE CHARACTERISTICS
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US94-02552-1

Query Match 100.0%; Score 20; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEP 4
DB 7 VLEP 10

RESULT 12
US-09-092-279B-504
; Sequence 504, Application US/09092279B
; Patent No. 6259782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohmed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH PHRANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/092,279B
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 504
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence

Query Match 100.0%; Score 20; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-504

Query Match 100.0%; Score 20; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEP 4
DB 13 VLEP 16

RESULT 13
US-09-315-304B-504
; Sequence 504, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMA KINETIC
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 05/092,279
; PRIOR FILING DATE: 1994-04-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 504
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-504

Query Match 100.0%; Score 20; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEP 4
DB 13 VLEP 16

RESULT 14
US-09-314-268-106
; Sequence 106, Application US/09314268
; Patent No. 6346377
; GENERAL INFORMATION:
; APPLICANT: Doorbar, John
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATIVE TO SCREENING FOR INFLUENZA
; FILE REFERENCE: 3789/80902
; CURRENT APPLICATION NUMBER: US/09/314,268
; CURRENT FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: 09/314,269
; EARLIER FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 106
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Human papillomavirus type 30
US-09-314-268-106

Query Match 100.0%; Score 20; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 VLEP 4  
DB 19 VLEP 22

## RESULT 15

US-09-134-001C-4579  
; Sequence 4579, Application US/09134001C  
; Patent No. 6380370  
; APPLICANT: LYNN DOUCETTE-STAMM ET AL  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; FILE REFERENCE: GTC-007  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 4579  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4579

Query Match 100.0%, Score 20, DB 4, Length 70;  
Best Local Similarity 100.0%, Pred No 2.8e+02;  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VLEP 4  
DB 24 VLEP 27

## RESULT 16

US-09-134-001C-4579  
; Sequence 4579, Application US/09134001C  
; Patent No. 6380370  
; APPLICANT: LYNN DOUCETTE-STAMM ET AL  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; FILE REFERENCE: GTC-007  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 4579  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4579

Query Match 100.0%, Score 20, DB 4, Length 70;  
Best Local Similarity 100.0%, Pred No 2.8e+02;  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VLEP 4  
DB 42 VLEP 45

## RESULT 17

US-08-928-383B-13  
; Sequence 13, Application US/08928483B  
; Patent No. 6210921  
; APPLICANT: ROBERT W. FINBERG, JEFFREY M. BERGELSON,  
; TITLE OF INVENTION: COXSAKIEVIRUS AND ALONOVIRUS  
; FILE REFERENCE: PCT/US 97/00211  
; CURRENT FILING DATE: 1997-01-02  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 26  
; SEQ ID NO 13  
; LENGTH: 65  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
US-08-928-383B-13

Query Match 100.0%, Score 20, DB 4, Length 65;  
Best Local Similarity 100.0%, Pred No 3.2e+02;  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02106  
COMPUTER READABLE FORM  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent-In Release #1 0, Version #1 25  
CURRENT APPLICATION DATA: US/08/928,383B  
APPLICATION NUMBER: US/08/928,383B  
FILING DATE: 12-SEP-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/026,100  
FILING DATE: 13-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: DPN-020  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)742-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 75 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-928-383B-13

Query Match 100.0%, Score 20, DB 4, Length 75;  
Best Local Similarity 100.0%, Pred No 3e+02;  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VLEP 4  
DB 23 VLEP 26

## RESULT 18

US-09-655-270A-25  
; Sequence 25, Application US/09655270A  
; Patent No. 6329151  
; APPLICANT: ROUVIERE, PIERRE E.  
; TITLE OF INVENTION: High Density Sampling of Differentially Expressed Proteins  
; FILE REFERENCE: R01011 US NA  
; CURRENT FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: US/09/655,270A  
; PRIOR FILING DATE: 1999-February-19  
; PRIOR APPLICATION NUMBER: 60/152,542  
; PRIOR FILING DATE: 1999-September-03  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 25  
; LENGTH: 82  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
US-09-655-270A-25

Query Match 100.0%, Score 20, DB 4, Length 82;  
Best Local Similarity 100.0%, Pred No 3.2e+02;  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VLEP 4  
DB 58 VLEP 61

RESULT 19  
 US-09-208-804-3  
 ? Sequence 3, Application US/09208804  
 ? Patent No. 6030826  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Au Young, Janice  
 ? TITLE OF INVENTION: NOVEL HUMAN PAPULIN LIKE PROTEIN  
 ? NUMBER OF SEQUENCES: 4  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ? STREET: 3174 Porter Drive  
 ? CITY: Palo Alto  
 ? STATE: CA  
 ? COUNTRY: USA  
 ? ZIP: 94304  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Diskette  
 ? COMPUTER: IBM Compatible  
 ? OPERATING SYSTEM: DOS  
 ? SOFTWARE: FastSeq for Windows Version 2.0  
 ? CURRENT APPLICATION DATA:  
 ? APPLICATION NUMBER: US/09/208,804  
 ? FILING DATE: Herewith  
 ? CLASSIFICATION:  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: 08/801,743  
 ? FILING DATE:  
 ? ATTORNEY/AGENT INFORMATION:  
 ? NAME: Billings, Lucy J.  
 ? REGISTRATION NUMBER: 36,749  
 ? REFERENCE/DOCKET NUMBER: PF 0217 US  
 ? TELECOMMUNICATION INFORMATION:  
 ? TELEPHONE: 415-855-0555  
 ? TELEFAX: 415-845-4166  
 ? TELEX:  
 ? INFORMATION FOR SEQ ID NO: 3:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 93 amino acids  
 ? TYPE: amino acid  
 ? STRANDEDNESS: single  
 ? TOPOLOGY: linear  
 ? IMMEDIATE SOURCE:  
 ? LIBRARY: GenBank  
 ? CLONE: 693800  
 ? US-09-208-804-3

Query March 100.0%; Score 20; DB 3; Length 93;  
 Best Local Similarity 100.0%; Freq No 3 Re.02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 VLEP 4  
 DB 71 VLEP 74

RESULT 20  
 US-08-801-743-3  
 ? Sequence 3, Application US/08801743  
 ? Patent No. 6037164  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Au-Young, Janice  
 ? TITLE OF INVENTION: NOVEL HUMAN PAPULIN LIKE PROTEIN  
 ? NUMBER OF SEQUENCES: 4  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ? STREET: 3174 Porter Drive  
 ? CITY: Palo Alto  
 ? STATE: CA  
 ? COUNTRY: USA  
 ? ZIP: 94304  
 ? COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/801,743  
 FILING DATE: Herewith  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J.  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PF-0217 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-845-4166  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 93 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: GenBank  
 CLONE: 693800  
 US-08-801-743-3

Query March 100.0%; Score 20; DB 3; Length 93;  
 Best Local Similarity 100.0%; Freq No 3 Re.02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4  
 DB 71 VLEP 74

RESULT 21  
 US-08-478-097A-5  
 ? Sequence 5, Application US/08478097A  
 ? Patent No. 6040431  
 ? GENERAL INFORMATION:  
 ? APPLICANT: KECK, PETER  
 ? APPLICANT: SMART, JOHN  
 ? TITLE OF INVENTION: SINGLE-CHAIN ANALOGS OF TGF-B  
 ? TITLE OF INVENTION: SUPERFAMILY (MORPHONS)  
 ? NUMBER OF SEQUENCES: 45  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HENFELD &  
 ? ADDRESS: THIBEAULT, LLP  
 ? STREET: 125 HIGH STREET  
 ? CITY: BOSTON  
 ? STATE: MA  
 ? COUNTRY: USA  
 ? ZIP: 02110  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Floppy disk  
 ? COMPUTER: IBM PC compatible  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: Patent Release #1.0, Version #1.05  
 ? CURRENT APPLICATION DATA:  
 ? APPLICATION NUMBER: US/08/478,097A  
 ? FILING DATE:  
 ? CLASSIFICATION: 530  
 ? ATTORNEY/AGENT INFORMATION:  
 ? NAME: PITCHER ESO, EDMOND R  
 ? REGISTRATION NUMBER: 27,829  
 ? REFERENCE/DOCKET NUMBER: GPP-080  
 ? TELECOMMUNICATION INFORMATION:  
 ? TELEPHONE: 617-248-7000  
 ? TELEFAX: 617-248-7100

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; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1-98
; OTHER INFORMATION: /note="TGF-R5 SEQUENCE"
US-08-478-097A-5

Query Match 100.0% Score 20; DB 3; Length 98;
Best Local Similarity 100.0%; Pred No 4; 1-02,
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 68 VLEP 71

RESULT 22
US-08-963-601-2
; Sequence 2, Application US/08963601
; Patent No. 5939528
; GENERAL INFORMATION:
; APPLICANT: CLAPPY, JIM C
; APPLICANT: CHOI, JUNGWON
; TITLE OF INVENTION: CRYSTALLINE FGF COMPLEX
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: APIAD Pharmaceuticals, Inc.
; STREET: 26 Lansdowne Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139-4234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1 0, Version #1 30
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/963,601
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/735,848
; FILING DATE:
; APPLICATION NUMBER: US 60/005,408
; FILING DATE: 23-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/006,069
; FILING DATE: 24-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BERNSTEIN, David L
; REGISTRATION NUMBER: 31,235
; REFERENCE/DOCYET NUMBER: AFIAD 350A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-494-0400
; TELEFAX: 617-494-0208
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-963-601-2

Query Match 100.0% Score 20; DB 2; Length 100;
Best Local Similarity 100.0%; Pred No 4; 1-02,
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 68 VLEP 71

RESULT 23
US-08-488-551B-639
; Sequence 639, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-8299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM321/95
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCYET NUMBER: 96062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 639:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-488-551B-639

Query Match 100.0% Score 20; DB 3; Length 105;
Best Local Similarity 100.0%; Pred No 4; 1-02,
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 84 VLEP 87

RESULT 24
US-08-388-353-639
; Sequence 639, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
```

APPLICANT: Learmont, Jennifer C.  
APPLICANT: McPhee, Dale A.  
APPLICANT: Crowe, Suzanne  
APPLICANT: Cooper, David  
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV 1  
NUMBER OF SEQUENCES: 800  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Prosser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/100,353  
FILING DATE: 14-FEB-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9606  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 639:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-388-353-639

Query Match 100.0%; Score 20; DB 3; Length 108;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4  
DB 84 VLEP 87

RESULT 25  
US-08-927-433-7  
Sequence 7, Application US/08927433  
Patent No. 6107476  
GENERAL INFORMATION:  
APPLICANT: Erlander, Mark G.  
APPLICANT: Huang, Shaoming  
APPLICANT: Jackson, Michael A.  
APPLICANT: Peterson, Per A.  
TITLE OF INVENTION: INHIBITING GROWTH FACTOR FOR TREATING PROSTATE CANCER, AND RELATED  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Johnson & Johnson  
STREET: One J & J Plaza  
CITY: New Brunswick  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 08933  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/927,433

FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Morrison, Alan J.  
REGISTRATION NUMBER: 37,399  
REFERENCE/DOCKET NUMBER: OPT-849  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-524-3592  
TELEFAX: 732-524-2808  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 112 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-927-433-7

Query Match 100.0%; Score 20; DB 3; Length 112;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4  
DB 82 VLEP 85

Search completed: March 5, 2003, 08:34:35  
Job time : 15 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: March 5, 2003, 08:37:36, Search time 15 seconds  
(without alignments)  
25.636 Million cell updates/sec

Title: US-09-732-411-15

Perfect score: 20

Sequence: 1 VLEP 4

Scoring table: BLQSUM62

Gapop 10.0, Gapext 0.5

Searched: 281224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 86

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database: PIR 73.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	60.0	3	A33802	thyrotropin-releas
2	11	55.0	4	I51049	metallothionein-A
3	10	50.0	4	P44A23	synaptosomal assoc
4	8	40.0	4	A02147	phagocytosis-stimu
5	7	35.0	3	RHTD70	thyroliberin - Bom
6	7	35.0	3	RHPGT	thyroliberin - pig
7	7	35.0	3	RHSHT	thyroliberin - she
8	7	35.0	3	A92971	thyroliberin - eas
9	7	35.0	3	A43391	TRH-like tripeptid
10	7	35.0	3	A17890	tyrosine protein k
11	7	35.0	4	A32019	tyrosine melanocyt
12	7	35.0	4	P00140	carbon-monoxide de
13	7	35.0	4	A61300	22K superhelical D
14	7	35.0	4	I57745	D-mannosyl hydrol
15	7	35.0	4	S53508	sarvalstatin-induced
16	7	35.0	4	S17255	ribosomal protein
17	7	35.0	4	A34626	PPCH-related neuro
18	7	35.0	4	PT0240	lg heavy chain cnp
19	7	35.0	4	I54357	schwannomin - mous
20	7	35.0	4	PT0675	T-cell receptor be
21	6	30.0	4	A48360	gamma subunit of p
22	6	30.0	4	A27897	glucan 1,4-alpha-g
23	5	25.0	4	A41890	protein D - Escher
24	5	25.0	4	B43848	cell surface adhes
25	5	25.0	4	I40505	hypothetical prote
26	5	25.0	4	PT0677	T-cell receptor be
27	5	25.0	4	A56209	protein glutamine
28	5	25.0	4	S55238	pallidipin - assas
29	4	20.0	3	P00010	angiotensin-conver

#### ALIGNMENTS

##### RESULT 1

A33802

thyrotropin-releasing hormone-like peptide - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 15-Jun-2001 #sequence\_revision 15 Jun 2001 #text\_change 15-Jun 2001

C:Accession: A33802

P:Coekle, S.M.; Aitken, A.J.; Bej, F.; Smyth, D.G.

J Biol Chem 264, 7788-7791, 1989

A:Title: A novel peptide, pyroglutamylglutamyproline amide, in the rabbit prostatic comp

A:Reference name: A33802, WHIS 245136, PIR:149405

A:Accession: A33802

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-3 <COC>

C:Superfamily: unassigned animal peptides

C:Keywords: amidated carboxyl end, pyroglutamic acid

F1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

F3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match: 60.0% Score 12; DB 3; Length 3;  
Best Local Similarity 100.0%, Pred No 2.8e+05; Mismatches 0; Gaps 0;  
Matches 2; Conservative 0; Indels 0; Gaps 0;

QY 3 EP 4

DB 2 EP 3

##### RESULT 2

I51049

metallothionein-A - rainbow trout (fragment)

C:Species: Oncorhynchus mykiss (rainbow trout)

C:Date: 13-Sep-1994 #sequence\_revision 13-Sep-1994 #text\_change 21-Jul-2000

C:Accession: I51049

P:Olsson, P.E.; Flind, P.; Erkel, L.J.; Kille, P.

Eur J Biochem 230, 344-349, 1995

A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss)

A:Reference number: I51049; MUID:95324545; PMID:7601121

A:Accession: I51049

A>Status: preliminary, translated from ORF/EMBL/CDDB

A:Molecule type: DNA

A:Residues: 1-4 <CDS>

A:Cross-references: EMBL:X60181; NID:G1019799; PIR:CAA56466.1; PIR:04370328

Query Match

Best Local Similarity 95.0%, Score 11; DB 2; Length 4;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4  
: :  
DB 1 MDP 3

## RESULT 3

E44823  
synaposomal-associated protein SNAP-25 peptide 1 - rabbit (fragment)  
N:Alternate names: superprotein peptide 1  
C:Species: *Oryctolagus cuniculus* (domestic rabbit)  
C:Date: 31-Mar-1993 #sequence\_revision 18 Nov-1994 #text\_change 15-Jun-1996

C:Accession: E44823

R:Cooney, A.; Liu, W.S.; Baittinger, C.; Willard, M.B.

J. Neurosci. 11, 3412-3421, 1991

A:Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is

A:Reference number: A44823; MUID:9204785; PMID:1941090

A:Accession: E44823

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-4 <DOB>

A:Experimental source: visual tissue

A:Note: sequence extracted from NCBI backbone (NCBIP:64247)

C:Keywords: membrane trafficking

Query Match 50.0%; Score 10; DB 2; Length 4;

Best Local Similarity 33.3%; Pred No. 2.9e+05;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3  
: :  
DB 1 IME 3

## RESULT 4

A02147

phagocytosis-stimulating peptide (tuftsin) - human

C:Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 01-Feb-1994

C:Species: *Homo sapiens* (man)

C:Accession: A02147

R:Kishimoto, A.; Kishimoto, A.; Satoh, F.S.; Nijjar, V.A.

Biochem. Biophys. Res. Commun. 47, 172-179, 1972

A:Title: The characteristics, isolation and synthesis of the phagocytosis stimulating pe

A:Reference number: A02147; MUID:7014790; PMID:4112769

A:Accession: A02147

A:Molecule type: protein

A:Residues: 1-4 <NIS>

A:Note: a peptide having the same structure, physical properties, and biological activity

R:Fidalgo, B.V.; Nijjar, V.A.

Biochemistry 6, 3386-3392, 1967

A:Reference number: A77602; MUID:6001045; PMID:410272

A:Contents: annotation; immunoglobulin class

C:Comment: An IgG (called leucokinin) binds reversibly to the cell membrane of neutrophils

n is essential for maximum stimulation of the phagocytic activity of neutrophils

C:Superfamily: immunoglobulin C region, immunoglobulin homology

Query Match 40.0%; Score 8; DB 2; Length 4;

Best Local Similarity 50.0%; Pred No. 2.9e+05;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EP 4  
: :  
DB 2 KP 3

## RESULT 5

A02147

thyroliberin - *Bombina orientalis*

C:Species: *Bombina orientalis*

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C:Accession: A02147

R:Yasuhara, T.; Nakajima, T.

Chem Pharm Bull 33, 2011-2013, 1975

A:Title: Occurrence of Pyr-His-Pro-NH-2 in the frog skin.

A:Reference number: A90919; MUID:7614399; PMID:815011

A:Accession: A90919

A:Molecule type: protein

A:Residues: 1-3 <YAS>

C:Superfamily: thyroliberin precursor

C:Keywords: amidated carboxyl end; cutaneous gland; hormone; pyroglutamic acid

F1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

F3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 35.0%; Score 7; DB 3; Length 3;

Best Local Similarity 100.0%; Pred No. 2.9e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4  
DB 3 P 3

## RESULT 6

RHPGT

thyroliberin - pig

C:Species: *Sus scrofa domestica* (domestic pig)

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C:Accession: A01415

P:Nair, R.M.G.; Barrett, J.F.; Powers, C.V.; Schally, A.V.

Biochemistry 9, 1103-1106, 1970

A:Title: Structure of porcine thyrotropin-releasing hormone.

A:Reference number: A90560; MUID:7013150; PMID:498498

A:Accession: A01415

A:Molecule type: protein

A:Residues: 1-3 <NAI>

R:Polier, J.; Fournier, F.; Folkers, K.; Schally, A.V.

Biochem. Biophys. Res. Commun. 37, 705-710, 1969

A:Title: The identity of chemical and hormonal properties of the thyrotropin-releasing ho

A:Reference number: A90167; MUID:70039904; PMID:4982117

A:Contents: annotation

A:Note: biological activities and Rf values (in 10 chromatographic systems) of the synth

C:Superfamily: thyroliberin precursor

C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid

F1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

F3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 35.0%; Score 7; DB 3; Length 3;

Best Local Similarity 100.0%; Pred No. 2.9e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4  
DB 3 P 3

## RESULT 7

RHSHT

thyroliberin - sheep

C:Species: *Ovis orientalis aries*, *Ovis ammon aries* (domestic sheep)

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C:Accession: A93750; A01415

R:Residues: 1-3 <F.M., Borjas, F.; Dunn, T.F.; Vale, W.; Guillemin, R.; Ward, D.M.

Org. Mass Spectrom. 5, 201-208, 1971

A:Title: The elucidation of the primary structure of the hypothalamic thyroid stimulating

A:Reference number: A93750

A:Accession: A93750

A:Molecule type: protein

A:Residues: 1-3 <DES>

R:Auragus, P.; Dunn, T.F.; Residues, P.; Vale, W.; Guillemin, R.

Nature 226, 321-325, 1970

A:Title: Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor.

A:Reference number: A93161; MUID:70163386; PMID:4985794

A:Contents: annotation

A:Note: physicochemical characteristics and biological activities of the natural and syn

C:Superfamily: thyroliberin precursor

C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid



F1/Modified site: pyroglutamic carboxylic acid (Gln) #status experimental  
F3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 35.0%; Score 7; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred No 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4  
|  
DB 3 P 3

## RESULT 8

A02971  
A:Title: thyroliberin - eastern newt (tentative sequence)  
C:Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)  
C:Date: 15-Jun-2001 #sequence\_revision 15 Jun-2001 #text\_change 15 Jun-2001  
C:Accession: A02971; A01415  
R:Grimm-Jorgensen, Y.; McKelvey, J.F.  
J. Neurochem. 23, 471-478, 1974  
A:Title: Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain  
A:Reference number: A02971; MUIP:75035605; PMID:4214538  
A:Accession: A02971  
A:Molecule type: protein  
A:Residues: 1-3 <GB1>  
A:Note: a peptide with the chemoattractant and electrophoretic characteristics of thyroliberin, or glutamic acid  
C:Superfamily: thyroliberin precursor  
C:Keywords: amidated carboxyl end; cutaneous gland; hormone; hypothalamus; pyroglutamic  
F1/Modified site: pyroglutamic carboxylic acid (Gln) #status experimental  
F3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 35.0%; Score 7; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred No 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4  
|  
DB 3 P 3

## RESULT 9

A43391  
A:Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroglutamic acid, from alfalfa  
C:Species: Medicago sativa (alfalfa)  
C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15 Jun-2001  
C:Accession: A43391  
R:Lackey, D.B. 267, 17508-17511, 1992  
J. Biol. Chem. 267, 17508-17511, 1992

A:Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroglutamic acid, from alfalfa  
C:Species: Medicago sativa (alfalfa)  
C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15 Jun-2001  
C:Accession: A43391  
A:Molecule type: protein  
A:Residues: 1-3 <LAC>  
C:Keywords: amidated carboxyl end; pyroglutamic acid  
F1/Modified site: pyroglutamic carboxylic acid (Gln) #status experimental  
F3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 35.0%; Score 7; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred No 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4  
|  
DB 3 P 3

## RESULT 10

I78890  
A:Title: tyrosine protein kinase - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C:Accession: I78890

F:Chow, R.M.; Davidson, E.J.; Fournel, M.; Gosselin, E.; Lemieux, S.; Tye, M.; Pozak, R.J. Oncogene 9, 3437-3448, 1994  
A:Title: Two distinct protein isoforms are encoded by *trk-4*, a *trk* related tyrosine protein kinase gene  
A:Reference number: I68487; MUIP:66666666; PMID:7470703  
A:Accession: I78890  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-3 <RES>  
A:Cross-references: GB:L33339, NID:G609536, FIDN:AAA64432.1; PID:G609538  
C:Genetics:  
C:Gene: p52ntk

Query Match 35.0%; Score 7; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred No 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4  
|  
DB 2 P 2

## RESULT 11

A32039  
A:Title: tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1: bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 31-Jul-1993 #sequence\_revision 31 Jul 1993 #text\_change 14-Aug-2000  
C:Accession: A32039  
R:Horvath, A.; Kastin, A.J.  
J. Biol. Chem. 268, 2175-2179, 1993  
A:Title: Isolation of tyrosine melanocyte-stimulating hormone release inhibiting factor 1  
A:Reference number: A32039; MUIP:99132295; PMID:12563371  
A:Accession: A32039  
A:Molecule type: protein  
A:Residues: 1-4 <HOR>  
A:Experimental source: brain  
C:Superfamily: unassigned animal peptides  
C:Keywords: amidated carboxyl end  
F1/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 35.0%; Score 7; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred No 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4  
|  
DB 2 P 2

## RESULT 12

PL0140  
A:Title: carbon-monoxide dehydrogenase (EC 1.2.3.20) large chain: Pseudomonas aeruginosa  
C:Species: Pseudomonas carboxydohydrogena  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 28-Apr-1993  
C:Accession: PL0140  
R:Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.  
Arch. Microbiol. 152, 335-341, 1989  
A:Title: Hemeology and distribution of carbon monoxide dehydrogenase in the cell cytoplasm  
A:Reference number: PL0140; MUIP:00055679; PMID:2418128  
A:Accession: PL0140  
A:Molecule type: protein  
A:Residues: 1-4 <KRA>  
C:Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, medium, and small

Query Match 35.0%; Score 7; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred No 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4  
|  
DB 4 P 4

## RESULT 13

A61300  
2XK superhelical DNA binding protein - Escherichia coli (fragment)  
C:Species: Escherichia coli  
C:Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 07-May-1999  
C:Accession: A61300  
R:Kishi, F.; Elina, Y.; Miki, T.; Nakazawa, T.; Nakazawa, A.  
J. Biochem. 92, 1059-1068, 1982  
A:Title: Purification and characterization of a protein from Escherichia coli which forms a complex with superhelical DNA  
A:Reference number: A61300; PMID:8408496; PMID:6294062  
A:Accession: A61300  
A:Molecule type: protein  
A:Residues: 1-4 <KIS>  
C:Comment: This protein resembles some of the histone-like protein of bacteria in amino acid composition.  
C:Keywords: DNA binding, monomer

Query Match 35.0%; Score 7; DB 2; Length 4;  
Best Local Similarity 50.0%; Pred. No. 2 8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

QY 2 LE 3  
DB 1 ME 2

## RESULT 14

I57745  
D-mannanase hydrolase (uxuA) - Escherichia coli  
C:Species: Escherichia coli  
C:Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 08-Oct-1999  
C:Accession: I57745  
R:Blanco, C.; Ritzenthaler, F.; Kolb, A.  
Mol. Gen. Genet. 262, 112-119, 1986  
A:Title: The regulatory region of the uxuA gene in Escherichia coli K12  
A:Reference number: I57745; PMID:86374344; PMID:3083215  
A:Accession: I57745  
A:Status: preliminary, translated from GE/EMBL/DBCP  
A:Molecule type: DNA  
A:Residues: 1-4 <EE>  
A:Cross-references: EMBL X03411, NID 943309, RDN CAC0147 1, FID:J581054

Query Match 35.0%; Score 7; DB 2; Length 4;  
Best Local Similarity 50.0%; Pred. No. 2 8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

QY 2 LE 3  
DB 1 ME 2

## RESULT 15

S53508  
starvation-induced ribonuclease - tomato  
C:Species: Lycopersicon esculentum (tomato)  
C:Date: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 07-May-1999  
C:Accession: S53508  
R:Koeck, M.; Loeffler, A.; Abel, S.; Glund, K.  
Plant Mol. Biol. 27, 477-485, 1995  
A:Title: cDNA structure and regulatory properties of a family of starvation-induced ribonucleases  
A:Reference number: S53506; PMID:9520142; PMID:7934213  
A:Accession: S53508  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-4 <KOE>

Query Match 35.0%; Score 7; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2 8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 4 P 4  
DB 2 F 2

## RESULT 16

S17255  
ribosomal protein Yml1, mitochondrial, questionable - yeast (Saccharomyces cerevisiae)  
C:Species: Saccharomyces cerevisiae  
A:Variety: strain 07173  
C:Date: 23-Apr-1991 #sequence\_revision 14-Sep-1994 #text\_change 09-May-1997  
C:Accession: S17255  
R:Grohmann, L.; Graack, H.P.; Kruff, V.; Choli, T.; Goldschmidt-Reisin, S.; Kitakawa, M.  
FEBS Lett. 294, 51-56, 1991  
A:Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit from yeast  
A:Reference number: S17255; PMID:2128100; PMID:2560626  
A:Accession: S17255  
A:Molecule type: protein  
A:Residues: 1-4 <GPO>  
C:Comment: A coding region for this protein could not be identified in the genome of Saccharomyces cerevisiae.  
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 35.0%; Score 7; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2 8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 4 P 4  
DB 4 P 4

## RESULT 17

A34626  
RPM1-related neurotrophin - ferruginous spindle  
C:Species: Fusinus ferrugineus (ferruginous spindle)  
C:Date: 02-Jul-1992 #sequence\_revision 02-Jul-1992 #text\_change 21-Dec-1993  
C:Accession: A34626  
R:Kobayashi, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.  
Biochem. Biophys. Res. Commun. 167, 773-778, 1990  
A:Title: A molluscan neurotrophin related to the crustacean hormone, RPCH.  
A:Reference number: A34626; PMID:20179762; PMID:2310194  
A:Accession: A34626  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-4 <RDP>  
C:Keywords: neurotrophin

Query Match 35.0%; Score 7; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2 8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 4 P 4  
DB 2 P 2

## RESULT 18

PT0240  
Ig heavy chain CRO3 region (clone 2-100B) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 20-Sep-1993 #sequence\_revision 20-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0240  
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Garon, A.J.; Povera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and joining segments in the CRO3 region of a human B cell clone.  
A:Reference number: PT0240; PMID:91109327; PMID:1899102  
A:Accession: PT0240  
A:Molecule type: DNA  
A:Residues: 1-4 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 35.0%; Score 7; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2 8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

A; Residues: 1-4 <CAP>  
A; Cross-references: GP 881987; MID-G245213; PIDN-AB2139113; PID-G245214  
A; Note: sequence extracted from NCBI backbone (NR01-61987, NCBI-P1912)

Query Match 30.0%; Score 6; DB 2; Length 4;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	2 LE 3
Ed	2 LQ 3

## RESULT 22

A37897  
Glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - *Aspergillus phoenicis* (fragment)  
NAlternate names: glucoamylase  
CSpecies: *Aspergillus phoenicis*  
CDate: 16-Aug-1988 #sequence revision 16-Aug-1988 #exchange 06-Nov-1996  
CAccession: A37897  
EInokuchi, N.; Takahashi, T.; Irie, M.

J. Biochem. 90, 1065-1067, 1981  
A. Title: Purification and Characterization of a Minor Glucosylase from *Aspergillus niger*  
A. Reference number: A27897; MUID:82075730; PMID:6796592

A; Accession: A2  
A; Molecule type:  
A; Residues: 1-4

Query M...

Best Local Similarity 50.0%; Prod No. 2 86.05;  
Matches 1; Conservative 1; Mismatches 0; Indels 2; Gaps 0

```

CSP: 1942 was masculus (mouse mouse)
C.Date: 17-Jul-1942 #sequence_revision 17 Jul 1942 #text_change 30-May-1997
C.Accession: PT0675
R: Feeney, A. J.

```

J. Exp. Med. 174, 115-124, 1991  
A.Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A.Reference number: PTD09; MID-91277601; PMID-1711554

A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-4 <FE>  
A:Experimental source: 400 18 fetal thymus  
A:Experimental source: 400 18 fetal thymus

Quantity	March	35.00	Score	7	DB	27	Length	4
Keywords:	T-cell	receptor						

Best Local Similarity	100.0%	Pred No 2	88.05
Matches	1	Conservative	0
		Mismatches	0
		Indels	0
		Gaps	0

RESULT 21  
A48360  
gamma subunit of, Protein A - Methylosinus trichosporium (fragment)

C-species: Methylinosinus trichosporium  
C-date: 19-Nov-1993 #sequence\_revision  
C-accession: A48360  
P-cardy: P. J. Laidler, V. J. Salmend, C. P. Murrell, J. C. P. Cardy, P. J. Laidler, V. J. Salmend, C. P. Murrell, J. C. P. Cardy

A1:Title: The methane monooxygenase gene cluster of *Methylosinus trichosporium*: cloning  
A1:Reference number: A4836; MED:92161931; PMID:1740954  
A1:Contents: OB3b

A.Accession: A48360  
A.Status: preliminary  
A.Molecule type: DNA

\_\_\_\_\_

A:Reference number: A43848; MUID:9217606; PMID:1541563

A:Accession: B43848

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-4 <LIA>

A>Note: sequence extracted from NCBI Backbone (NCBI:85444)

Query Match 25.0%; Score 5; DB 2; Length 4;  
Best Local Similarity 50.0%; Pred No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2  
:  
Db 1 ML 2

# RESULT 25

I40505

hypothetical protein 3 (4 aa) - Bacillus stearothermophilus

C:Species: Bacillus stearothermophilus

C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 15-Oct-1999

C:Accession: I40505

P:Waye, M M ; Winter, G

Eur. J. Biochem. 188, 505-510, 1986

A:Title: A transcription terminator in the 5' non-coding region of the tyrosyl tRNA synthetase gene of Bacillus stearothermophilus

A:Reference number: I40505, MUID:86074732; PMID:3522162

A:Accession: I40505

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-4 <RES>

A:Cross-references EMBL X04193; NID:G40233; PION:OAA07793.1, PID:9580944

Query Match 25.0%; Score 5; DB 2; Length 4;  
Best Local Similarity 50.0%; Pred No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2  
:  
Db 1 ML 2

Search completed: March 5, 2003, 09:40:49  
Job time : 16 secs



```
13. Mass Spectrom. 5:221-228 (1971).
RN [4]
RP SYNTHESIS.
RC SPECIES=Sheep;
RX MEDLINE=70163386; PubMed=4985794;
RA Burges P., Dunn T F., Desiderio D M., Ward D N., Vale W.,
RA Guillemin R.
RT "Characterization of ovine hypothalamic hypophysiotropic
RT TSH-releasing factor."
RL Nature 228:321-325 (1978).
RN [5]
RP SEQUENCE.
RC SPECIES=B. orientalis; TISSUE=SKIN;
RX MEDLINE=76138399; PubMed=815011;
RA Yasuhara T., Nakajima T.,
RA "Letter: Occurrence of Pyr-His-Pro-Gly2 in the frog skin ";
RL Chem. Pharm. Bull. 23:3301-3303 (1976)
RN [6]
RP SEQUENCE.
RC SPECIES=N. viridescens;
RX MEDLINE=7535605; PubMed=4214528,
RA Grim J., Jensen Y., Nefelky J.F.,
RT "Biosynthesis of thyrotropin releasing factor by newt (Triturus
RT viridescens) brain in vitro. Isolation and characterization of
RT thyrotropin releasing factor."
RL J. Neurochem. 23:471-478 (1974)
RC "FUNCTIONAL TSH FRAGMENTS AS A REGULATOR OF THE BIOSYNTHESIS OF TSH
RC IN THE ANTERIOR PITUITARY GLAND AND AS A NEUROTRANSMITTER/
RC NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS."
RC PIR; A01415; RHPGT.
DE PIR; A93750; PHSHT.
DE LIF; A96913; PHSTED.
DE PIR; A92971; A92971.
RN Amidation.
FT MOD RES 1 1 PEP-ULINIC CARBOXYLIC ACID
FT MOD RES 3 3 AMIDATION.
SQ SEQUENCE 3 AA, 360 MW, 7761560000000000 CRC64;

Query Match 35.0%, Score 7, DB 1, Length 3;
Best Local Similarity 100.0%; Pred. No. 1 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4
DB 3 P 3

RESULT 3
DCML_PSECH STANDARD; PPT; 4 AA.
AC P19916;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Carbin monoxide dehydrogenase large chain (EC 1.2.99.2) (CC
DE dehydrogenase subunit L) (CO-DH L) (Fragment).
GN CCTL.
CS Pseudomonas carboxydhydrogena.
CC Bacteria, Proteobacteria, Alpha subdivision, Enterobacteriaceae group.
CC Bradyrhizobium group.
OX NCBI_TaxID=290;
RN [1]
RP SEQUENCE.
FX MEDLINE=9005578; PubMed=2818139;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.
RT "Homology and distribution of CO dehydrogenase structural genes in
RT carboxydehydrogenic bacteria."
RL Arch. Microbiol. 163:336-341 (1994)
CC "Function: Catalyzes the oxidation of carbon monoxide to carbon
CC dioxide.
CC CATALYTIC ACTIVITY CO + H2O + acceptor -> CO2 + reduced
CC acceptor.
CC "REACTING MOLYBDENUM (molybdopterin)

13. Mass Spectrom. 5:221-228 (1971).
RN [4]
RP SYNTHESIS.
RC SPECIES=Sheep;
RX MEDLINE=70163386; PubMed=4985794;
RA Burges P., Dunn T F., Desiderio D M., Ward D N., Vale W.,
RA Guillemin R.
RT "Characterization of ovine hypothalamic hypophysiotropic
RT TSH-releasing factor."
RL Nature 228:321-325 (1978).
RN [5]
RP SEQUENCE.
RC SPECIES=B. orientalis; TISSUE=SKIN;
RX MEDLINE=76138399; PubMed=815011;
RA Yasuhara T., Nakajima T.,
RA "Letter: Occurrence of Pyr-His-Pro-Gly2 in the frog skin ";
RL Chem. Pharm. Bull. 23:3301-3303 (1976)
RN [6]
RP SEQUENCE.
RC SPECIES=N. viridescens;
RX MEDLINE=7535605; PubMed=4214528,
RA Grim J., Jensen Y., Nefelky J.F.,
RT "Biosynthesis of thyrotropin releasing factor by newt (Triturus
RT viridescens) brain in vitro. Isolation and characterization of
RT thyrotropin releasing factor."
RL J. Neurochem. 23:471-478 (1974)
RC "FUNCTIONAL TSH FRAGMENTS AS A REGULATOR OF THE BIOSYNTHESIS OF TSH
RC IN THE ANTERIOR PITUITARY GLAND AND AS A NEUROTRANSMITTER/
RC NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS."
RC PIR; A01415; RHPGT.
DE PIR; A93750; PHSHT.
DE LIF; A96913; PHSTED.
DE PIR; A92971; A92971.
RN Amidation.
FT MOD RES 1 1 PEP-ULINIC CARBOXYLIC ACID
FT MOD RES 3 3 AMIDATION.
SQ SEQUENCE 3 AA, 360 MW, 7761560000000000 CRC64;

Query Match 35.0%, Score 7, DB 1, Length 4;
Best Local Similarity 100.0%; Pred. No. 1 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4
DB 4 P 4

RESULT 5
EOSI HUMAN STANDARD; PPT; 4 AA.
AC P02731;
DT 21-JUN-1986 (Rel. 01, Created)
DT 21-JUN-1986 (Rel. 01, Last sequence update)
DT 21-JUN-1986 (Rel. 01, Last annotation update)
DE Eosinophilotoxic peptides.
CS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; HOMO.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
PX MEDLINE=76078412; PubMed=1060093;
RA Garziz E J., Austen K.F.;
RT "Purification and synthesis of eosinophilic toxic peptide of
RT human lung tissue: Identification as eosinophil chemotactic factor of
RT anaphylaxis".
RL PNAS. 81:11. Acad. Sci. U.S.A. 72:4193-4197 (1984)
CC "MISCELLANEOUS. THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG
```

CC (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS  
 CC (ANAPHYLAXIS) THEIR ACTIVITIES, PREFERENTIALLY AFFECTING  
 CC EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE  
 CC OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.

DR PIR; A03190; ETHU. 1 V -> A (IN OTHER PEPTIDE)  
 FT VARIANT 1  
 FT MOD\_RES 4 AA; 598 MW; 69058962A000000000 CRC64;  
 SQ SEQUENCE 4 AA; 598 MW; 69058962A000000000 CRC64;

Query Match 25.0%; Score 5; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred No 1.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 E 3  
 |  
 Db 4 E 4

## RESULT 6

FLRF\_HIRME STANDARD; PRT; 4 AA.  
 AC P42562;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRFamide-like neuropeptide YLRP-amide.  
 OS Hirudo medicinalis (medicinal leech).  
 CC Eukaryota; Metazoa; Annelida; Clitellaria; Hirudinida; Hirudinea;  
 CC Arynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo  
 CC NCBI\_TaxID=6421;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE=92195954; PubMed=1686933;  
 RA Evans R D., Pohl J., Kartsonis M A., Calabrese P L.;  
 RT "Identification of RFamide neuropeptides in the medicinal leech";  
 RL Peptides 12:897-908(1991).  
 CC -1- SIMILARITY: BELONGS TO THE FAPP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 4 4 AMIDATION.  
 FT MOD\_RES 4 AA; 598 MW; 6904071B3000000000 CRC64;  
 SQ SEQUENCE 4 AA; 598 MW; 6904071B3000000000 CRC64;

Query Match 20.0%; Score 4; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred No 1.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 L 2  
 |  
 Db 2 L 2

## RESULT 7

FLRF\_HIRME STANDARD; PRT; 4 AA.  
 AC P42561;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRFamide.  
 OS Hirudo medicinalis (medicinal leech), and  
 OS Helisoma trivolvis (Snail).  
 CC Fukuyama; Metazoa; Annelida; Clitellaria; Hirudinida; Hirudinea;  
 CC Arynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.  
 CC NCBI\_TaxID=6421, 27815;  
 RN [1]  
 RP SEQUENCE.

CC SPECIES=H. medicinalis;

EX MEDLINE=92195954; PubMed=1686933;

RA Evans R D., Pohl J., Kartsonis M A., Calabrese P L.;

RT "Identification of RFamide neuropeptides in the medicinal leech";

RL Peptides 12:897-908(1991).

RN [2]

RP SEQUENCE

FC SPECIES=H. trivolvis; TISSUE=Kidney;  
 EX MEDLINE 94296417; PubMed=7942428;  
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.P., Salomadin A.S.M.;  
 RT "FMRFamide-related peptides from the kidney of the snail, Helisoma  
 trivolvis";  
 RL Peptides 15:31-36(1994)  
 CC -1- SIMILARITY: BELONGS TO THE FAPP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 4 4 AMIDATION.  
 FT MOD\_RES 4 AA; 582 MW; 6464077A0000000000 CRC64;  
 SQ SEQUENCE 4 AA; 582 MW; 6464077A0000000000 CRC64;

Query Match 20.0%; Score 4; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred No 1.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 L 2  
 |  
 Db 2 L 2

## RESULT 8

FLRN\_AMEL STANDARD; PRT; 4 AA.  
 AC P58707;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Antho-FNamide.  
 CC Anthopleura elegantissima (Sea anemone).  
 CC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
 CC Nymnantheae; Actiniidae; Anthopleura.  
 CC NCBI\_TaxID=6110;  
 RN [1]  
 RP SEQUENCE, AND MASS-SPECTROMETRY.  
 EX MEDLINE=90319322; PubMed=1973545;  
 RA Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,  
 RA Peinscheid P.K., Northacker H.-P., Staley A.L.;  
 RT "Isolation of L-3-Phenylactyl-Lys-Arg-Asp-NH2 (Antho-FNamide), a sea  
 anemone neuropeptide containing an unusual amino-terminal blocking  
 group";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Neuron-specific.  
 CC -1- MASS SPECTROMETRY MW 549.3, METHOD=D-FAB.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 1 1 L-3-PHENYLACTYL.  
 FT MOD\_RES 4 4 AMIDATION.  
 FT MOD\_RES 4 AA; 549 MW; 6464072A0000000000 CRC64;  
 SQ SEQUENCE 4 AA; 549 MW; 6464072A0000000000 CRC64;

Query Match 20.0%; Score 4; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred No 1.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 L 2  
 |  
 Db 2 L 2

## RESULT 9

LUKE\_VIBFI STANDARD; PRT; 3 AA.  
 AC F24272;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Arc);  
 DE protein synthetase (Fragment).  
 GN LUKE.  
 OS Vibrio fischeri.  
 CC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrion.  
 CC NCBI\_TaxID=668;  
 RN [1]







OCPI OCTMI  
ID OCPI OCTMI STANDARD, PRT, 4 AA.  
AC P58648;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Cardioactive peptides Ocp-1/Ocp-2.  
OS Octopus minor (Octopus).  
OC Eukaryota, Metazoa, Mollusca, Cephalopoda, Colecoidea, Octopoda;  
OC Incirrata; Octopodidae; Octopus.  
OX NCBI\_TaxID=99766;  
RN [1]  
RS SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION  
RC TISSUE=Brain;  
RX MEDLINE=20336915; PubMed=10876044;  
RA Iwakoshi E., Hisada M., Minakata H.,  
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,  
RT Octopus minor";  
RL Peptides 21:623-630(2000).  
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and  
CC inotropic effects on the heart. Ocp-2 is a 1000 time less  
CC active than Ocp-1.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- PTM: Ocp-2 has 1 Phe instead of D-Phe.  
CC -!- MASS SPECTROMETRY MW=475.2, METH-C-MALDI.  
KW Hormone; D-amino acid.  
FT MOD\_RES 2 D-PHENYLALANINE.  
SQ SEQUENCE 4 AA, 394 MW, 6AA879C810C0C0C0C CRC64;  
  
Query Match 10.0%; Score 2; DB 1; Length 4;  
Best Local Similarity 0.0%; Pred.No. 1.1e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 E 3  
DB 4 D 4

RESULT 16  
OCPI OCTMI  
ID OCPI OCTMI STANDARD, PRT, 4 AA.  
AC P58649;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Cardioactive peptides Ocp-3/Ocp-4.  
OS Octopus minor (Octopus).  
OC Eukaryota, Metazoa, Mollusca, Cephalopoda, Colecoidea, Octopoda;  
OC Incirrata; Octopodidae; Octopus.  
OX NCBI\_TaxID=99766;  
RN [1]  
RS SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.  
RC TISSUE=Brain;  
RX MEDLINE=20336915; PubMed=10876044;  
RA Iwakoshi E., Hisada M., Minakata H.,  
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,  
RT Octopus minor";  
RL Peptides 21:623-630(2000).  
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and  
CC inotropic effects on the heart. Ocp-4 is a 1000 time less  
CC active than Ocp-3.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- PTM: Ocp-4 has D-Ser instead of L-Ser.  
CC -!- MASS SPECTROMETRY MW=395.2, VETMO-MALDI.  
KW Hormone; D-amino acid.  
FT MOD\_RES 2 D-SERINE (IN OCP-4).  
SQ SEQUENCE 4 AA, 463 MW, 6AR3E5B1A0C0C0C0C CRC64;  
  
Query Match 10.0%; Score 2; DB 1; Length 4;  
Best Local Similarity 0.0%; Pred.No. 1.1e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 E 3

DB 4 D 4  
RESULT 17  
GRWM HUMAN  
ID GRWM HUMAN STANDARD, PRT, 3 AA  
AC P01157;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 21-JUL-1986 (Rel. 01, Last annotation update)  
DE Growth-modulating peptide.  
OS Homo sapiens (Human).  
OC Eukaryota, Metazoa, Chordata, Vertebrata; Pteridomorphi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RS SEQUENCE.  
RP MEDLINE=77162369; PubMed=858356;  
RA Schlesinger D.H., Pickart L., Thaler M.M.,  
RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine";  
RL Experientia 33:324-325(1977).  
CC -!- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE  
CC GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.  
DE PIR, A01421; OPHV  
SQ SEQUENCE 3 AA, 340 MW, 6311E1A10C0C0C0C0C CRC64;  
  
Query Match 5.0%; Score 1; DB 1; Length 3;  
Best Local Similarity 0.0%; Pred.No. 1.1e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 E 3  
DB 3 K 3

RESULT 18  
FFKA ANTEL  
ID FFKA ANTEL STANDARD, PRT, 4 AA.  
AC P58705;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Antho-KAamide  
OS Anthopleura elegantissima (Sea anemone).  
OC Eukaryota, Metazoa, Cnidaria, Anthozoa; Zoantharia; Actiniaria;  
OC Cnidaria; Actiniidae; Anthopleura.  
OX NCBI\_TaxID=6110,  
RN [1]  
RS SEQUENCE.  
RP MEDLINE=92028952; PubMed=1691803;  
RA McFarlane H.P., Finehart K.L. Jr., Grimmelikhuizen C.J.P.,  
RT "Isolation of L-3 phenylacetyl-Phe-Lys Ala-NH2 (Antho-KAamide), a  
RT novel neuropeptide from sea anemones";  
EL Biochem Biophys Res Commun 179:1205-1211(1991).  
RN [2]  
RS FUNCTION.  
RP MEDLINE=93301436; PubMed=8397415;  
PA McFarlane H.P., Hudman D., McFarlane H.P., Grimmelikhuizen C.J.P.,  
RT "The expansion behaviour of sea anemones may be coordinated by two  
RT inhibitory neuropeptides, Antho-KAamide and Antho-Ramide";  
FL Proc P Soc Lond, P, Biol Sci 363:183-188(1993).  
CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle  
CC groups. May be involved in the expansion phase of feeding  
CC behaviour in sea anemones.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Neuronal specific.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 1 L-3-PHENYLACETYL-  
FT MOD\_RES 4 4 AMIDATION.  
SQ SEQUENCE 4 AA, 512 MW, 6D03A0C0A0C0C0C0C CRC64;  
  
Query Match 5.0%; Score 1; DB 1; Length 4;

Best Local Similarity 0.0%; Pred No 1 le-05;  
Matches a; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 E 3  
Db 3 K 3

Search completed: March 5, 2003, 08:38:49  
Job time : 11 secs

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Genome version 5.1.3  
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OM protein : protein search, using sw model

Run on: March 5, 2003, 08:37:06 ; Search time 92 Seconds  
(without alignments)  
8 459 Million cell updates/sec

Title: US-09-732-411-15  
Perfect score: 20  
Sequence: 1 VLEP 4

Scoring table: BLASTM62  
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 286047115 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0  
Maximum DB seq length: 4

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Query			DB ID	Description
	Score	Match	Length		
1	9	45.0	4 11	Q08433	Q08433 rattus norv

#### SUMMARIES

RESULT 1  
Q08433  
ID Q08433 PRELIMINARY; PRT; 4 AA.  
AC Q08433;  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
DT 01-JAN-1999 (TRENBLrel. 09, Last annotation update)  
DE UDP-glucuronosyltransferase, microsomal (EC 2.4.1.17) (UDPGT)  
(Fragment).  
OS Rattus norvegicus (Rat).

#### ALIGNMENTS

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
CX R33\_732-411-15, 15  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GUNN;  
PA Sato H., Aono S., Fashiwamara S., Yoiwai O.,  
PT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the  
PL hyperbilirubinemic Gunn rat.", 177-1161-1164 (1991).  
CC R1 Biochem Biophys Res Commun 177:1161-1164 (1991).  
CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND  
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND  
CC ENDOGENOUS COMPOUNDS.  
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR -> UDP + ACCEPTEP  
CC -1- PETA-D-GLUCOPONOSIDE.  
CC -1- SUBCELLULAR LOCATION: MICROsome.  
DR EMBL; S38636; AAB19259.1; -.  
KW Transferase; Glycosyltransferase; Microsome; Multigene family.  
FT NON\_TER 1 1  
FT NON\_TER 4 4  
SQ SEQUENCE 4 AA; 473 MW; 633732042000000000 CFC64;  
Query Match 45.0%; Score 9; DB 11; Length 4;  
Best Local Similarity 66.7%; Pred No. 6.7e+04;  
Matches 2; Conservative 1; Mismatches 0; Gaps 0;  
QY 1 VLE 3  
DB 2 VLE 4

Search completed: March 5, 2003, 08:40:27  
Job time : 93 secs

the 1990s, the number of people in the UK who are aged 65 and over has increased by 1.5 million (1990–1999) and is projected to increase by a further 1.5 million by 2010 (Office for National Statistics 2000). The number of people aged 65 and over in the UK is projected to increase from 10.5 million in 1999 to 12.5 million in 2010, with the number of people aged 75 and over increasing from 4.5 million to 5.5 million in the same period (Office for National Statistics 2000). The increase in the number of people aged 65 and over is projected to be particularly marked in the 75–84 age range, with the number of people in this age range increasing from 1.5 million in 1999 to 2.5 million in 2010 (Office for National Statistics 2000).

There is a growing awareness of the need to address the health and social care needs of the ageing population. The Department of Health (2000) has identified the need to develop a 'new paradigm' of health and social care for the ageing population, which is based on the principles of 'active ageing' and 'lifespan care'. The 'new paradigm' is based on the idea that people should be able to live longer, healthier lives, and that health and social care should be provided in a way that is responsive to the needs of the ageing population. The 'new paradigm' is based on the following principles:

- People should be able to live longer, healthier lives.
- Health and social care should be provided in a way that is responsive to the needs of the ageing population.
- Health and social care should be provided in a way that is cost-effective.
- Health and social care should be provided in a way that is accessible to all.
- Health and social care should be provided in a way that is of high quality.

The 'new paradigm' is based on the idea that people should be able to live longer, healthier lives, and that health and social care should be provided in a way that is responsive to the needs of the ageing population. The 'new paradigm' is based on the following principles:

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- Health and social care should be provided in a way that is cost-effective.
- Health and social care should be provided in a way that is accessible to all.
- Health and social care should be provided in a way that is of high quality.

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- People should be able to live longer, healthier lives.
- Health and social care should be provided in a way that is responsive to the needs of the ageing population.
- Health and social care should be provided in a way that is cost-effective.
- Health and social care should be provided in a way that is accessible to all.
- Health and social care should be provided in a way that is of high quality.

OM protein - protein search, using sw model

Run on: March 5, 2003, 08:34:20, Search time 33 seconds  
(without alignments)  
16.152 Million cell updates/sec

Title: US-09-732 411-15

Perfect score: 20

Sequence: 1 VLRP 4

Scoring table: BLASTM62

Gapop: 10.0, Gapext: 0.5

Searched: 90470 seqs, 113250620 residues

Total number of hits satisfying chosen parameters: 11315

Minimum DR seq length: 0

Maximum DR seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database: A: Geneseq: joln02.\*

1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*

2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*

3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*

4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*

5: /SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*

6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*

7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*

8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*

9: /SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*

10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*

11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*

12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*

13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*

14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*

15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*

16: /SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*

17: /SID22/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*

18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*

19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*

20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*

21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*

22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*

23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	4	21	Chemotactic peptide
2	20	100.0	4	22	Adhesion-modulator
3	16	80.0	4	20	Interleukin 1 beta
4	14	70.0	4	20	Peptide used to ma
5	14	70.0	4	21	Chemotactic peptide
6	14	70.0	4	21	Granzyme B substra
7	14	70.0	4	21	Granzyme B substra
8	14	70.0	4	22	Fluorophore-label
9	14	70.0	4	22	Chicken bone deriv
10	14	70.0	4	22	Granzyme B peptide

11	14	70.0	4	22	Grasy, violet, mure
12	14	70.0	4	22	Escherichia coli r
13	14	70.0	4	23	Granzyme B peptide
14	14	70.0	4	23	Tumour associated
15	14	70.0	4	23	Tumour associated
16	14	70.0	4	23	Tumour associated
17	14	70.0	4	23	Tumour associated
18	14	70.0	4	23	Tumour associated
19	13	65.0	4	8	Immunomodulator po
20	13	65.0	4	11	ATP inhibitor pep
21	13	65.0	4	16	Antineoplastic pep
22	13	65.0	4	19	Human erythropoiet
23	13	65.0	4	20	Peptide used to ma
24	13	65.0	4	20	Human growth hormo
25	13	65.0	4	20	Human growth hormo
26	13	65.0	4	21	Fluorophore-label
27	13	65.0	4	21	Cathepsin B coll ad
28	13	65.0	4	22	Chicken bone deriv
29	13	65.0	4	22	Peptide which is u
30	12	60.0	4	23	Thyrotropin releas
31	12	60.0	3	16	Tripeptide having
32	12	60.0	3	19	Anti-inflammatory
33	12	60.0	3	21	Peptide used as an
34	12	60.0	4	5	Animal growth prom
35	12	60.0	4	5	Animal growth prom
36	12	60.0	4	5	Acetylcholinestera
37	12	60.0	4	9	Sequence of peptide
38	12	60.0	4	14	Diuretic hormone b
39	12	60.0	4	14	Diuretic hormone b
40	12	60.0	4	14	Diuretic hormone d
41	12	60.0	4	14	Diuretic hormone d
42	12	60.0	4	15	Oligopeptide deriv
43	12	60.0	4	16	Human growth hormo
44	12	60.0	4	16	Oligopeptide deriv
45	12	60.0	4	16	Immune stimulating
46	12	60.0	4	16	Terapeptide deriv
47	12	60.0	4	16	Terapeptide deriv
48	12	60.0	4	16	Terapeptide deriv
49	12	60.0	4	16	Peptide binding to
50	12	60.0	4	16	Peptidase substrat

## ALIGNMENTS

## RESULT 1

ID: AAB28663 standard; peptide; 4 AA.

XX AAB28663;

XX 13-PEB-2001 (first entry)

XX Chemotactic peptide pepJ'

XX Chemotactic; osteopontin; vulnery; antiarthritic; antiprosclerotic;

XX Chemotactic; antitumor; antiinflammatory; osteopathic;

XX Wound healing; cell migration; chemotaxis; atherosclerosis; cancer;

XX angiogenic-associated disease; arthritis; psoriasis; haemangioma;

XX ocular neovascularisation; cell apoptosis; nitrous oxide production;

XX inflammation; osteoporosis; immune disease.

XX Mammalia.

XX Synthetic.

XX W0200002247 A2.

XX PD 26-OCT-2000.

XX 17-APP-2000; 2000WO-US10344.

XX 15-APP-1999; 99US-0129764.

XX

PA (CHIL-) CHILDRENS MEDICAL CENT.  
 XX Ashkar S;  
 XX WPI: 2000-007159/47  
 XX  
 XX New osteopontin-derived chemotactic and inhibitory peptides, useful for  
 PT preventing scarless wound healing, modulating cellular chemotaxis,  
 PT treating formation of atherosclerotic plaques and preventing metastasis  
 PT  
 XX  
 PS Claim 17; Page 43; 54pp; English.  
 XX  
 CC The present sequence is an osteopontin-derived chemotactic peptide.  
 CC Such chemotactic peptides are useful for promoting scarless wound  
 CC healing, modulating chemotaxis and promoting cell migration to a target  
 CC site in a cell of a subject. They are also used for modulating cellular  
 CC chemotaxis in a mammalian cell such as smooth muscle cell, a macrophage,  
 CC an endothelial cell, a vascular cell and a tumorigenic cell. They are  
 CC useful for treating the formation of atherosclerotic plaques in a  
 CC subject. The peptides are used for preventing metastasis, treating an  
 CC angiogenic-associated disease such as arthritis, psoriasis, haemangioma,  
 CC tumour metastasis or ocular neovascularisation. They are also used for  
 CC activating cell apoptosis, for modulating nitrous oxide production and  
 CC for inducing chemotaxis. The peptides are useful for diagnosing, treating  
 CC and preventing tumour metastasis, inflammation, osteoporosis and immune  
 CC diseases. They can also be used to enhance an immune response by  
 CC attracting macrophages.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 20; DE 21; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLEP 4  
 Db ||||  
 1 VLEP 4  
 RESULT 2  
 AAB29558  
 ID AAB29558 standard; peptide; 4 AA.  
 XX  
 AC AAB29558;  
 XX  
 DT 14-FEB-2001 (first entry)  
 XX  
 DE Adhesion-modulatory peptide, SEQ ID NO:15.  
 XX  
 KW Adhesion modulatory peptide; target cell adhesion; cell adhesion;  
 KW endothelial cell; fibroblast; macrophage; neutrophil; myofibroblast;  
 KW collagen, glycosaminoglycan, extracellular matrix; synthetic substrate,  
 KW vascular growth; wound healing; keloid formation; scarring; fibrosis;  
 KW anti-infective; vulnervay; immunomodulatory; antibacterial; anticancer,  
 KW anti-tumorigenic; anti-CD44 activity; Prostheses; implants.  
 XX  
 OS Synthetic.  
 XX  
 PN W0200006324-A2  
 XX  
 PD 26-QT-2000  
 XX  
 XX 17-APP-2000; 2000WO 0510329.  
 PF  
 XX 16-APP-1999; 99US-0129709.  
 PP  
 XX (CHIL-) CHILDRENS MEDICAL CENT  
 PA  
 XX Ashkar S;  
 PI  
 XX WPI: 2001-007002/01  
 DR  
 XX

PT Novel adhesive modulatory peptides useful for modulating adhesion of  
 PT target cells such as endothelial cells, fibroblasts, macrophages to  
 XX substrate such as polyvinyl surfaces, collagen  
 XX  
 PS Claim 8; Page 27; 35pp; English.  
 XX  
 CC The invention relates to novel adhesion modulatory peptides (AAB29544-  
 CC AAB29558) which modulate the adhesion of a target cell to a substrate.  
 CC The invention also encompasses substrates and devices treated with a  
 CC peptide of the invention; compositions comprising a peptide of the  
 CC invention for in vivo use; and analogues, fragments and chemical  
 CC derivatives of the peptides of the invention. The peptides are useful for  
 CC modulating the adhesion to a substrate of target cells such as  
 CC myofibroblasts, fibroblasts, macrophages, neutrophils or  
 CC body of a patient, e.g., collagen or hyaluronic acid, or may be a  
 CC synthetic substrate e.g., a polyvinyl surface, titanium or PGA. The  
 CC peptides are useful for regulating vessel growth during wound healing  
 CC and/or in the treatment of damage resulting from vascular disease; for  
 CC inhibiting or preventing cellular apoptosis; in the treatment of  
 CC fibrosis, in particular in the clearing of debris; to minimise wound  
 CC contraction, thereby reducing keloid tissue formation and scarring; and  
 CC as anti clotting agents. The peptides also have an immunomodulatory  
 CC effect, and an antibacterial effect by adhering to neutrophils.  
 CC Additionally, peptides of the invention have an anticancer effect by  
 CC competing for alpha-v-beta3 integrin binding on the cell surface, and an  
 CC antitumorigenic effect by having anti-CD44 activity. The peptides are  
 CC useful for stimulating and/or enhancing cell attachment to polymer  
 CC scaffolds, to enhance tissue growth and for coating medical devices,  
 CC including prostheses and implants (e.g., vascular implants). The present  
 CC sequence represents a specifically claimed adhesion modulatory peptide of  
 CC the invention.  
 XX  
 SQ Sequence 4 AA,  
 Query Match 100.0%; Score 20; DE 22; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLEP 4  
 Db ||||  
 1 VLEP 4  
 RESULT 3  
 AAY03962  
 ID AAY03962 standard; peptide; 4 AA.  
 XX  
 AC AAY03962;  
 XX  
 DT 23-JUN-1999 (first entry)  
 XX  
 DE Interleukin-1 beta converting enzyme binding moiety.  
 XX  
 KW Cysteine protease inhibitor; exadiarole, thiadiazole, 1,2,4 triazole;  
 KW interleukin-1 beta converting enzyme inhibitor; IL-1; ICE; anti-tumor;  
 KW anticancer; antimicrobial; antibacterial; antiviral; anti-allergic;  
 KW anti-inflammatory; herbicide; fungicide; pesticide; multiple sclerosis;  
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;  
 KW ischaemic-reperfusion injury.  
 XX  
 OS Synthetic.  
 XX  
 PN WC9849100 A2.  
 XX  
 PD 05-NOV-1998.  
 XX  
 XX 24-APP-1998; 98WO-US08259  
 PF  
 XX 23-APP-1998; 98US-0044819  
 PP  
 XX 25-APP-1997; 97US-0044819.  
 XX  
 PA (COPT-) COPTTECH INC.



XX Cheronis JC, Gerrity JH, Goodfellow VS, Gyorkos AC;  
 PI Leimer AH, Spruce LW, Young JM;  
 XX WPI; 1999-131683/11.  
 XX New substituted oxadiazole cysteine protease inhibitors - useful  
 PT e.g. for inhibiting cancer cell growth, microbial cell or viral  
 PT growth or treating inflammatory and degenerative diseases  
 XX  
 PS Claims 61, 62; Pages 67, 68; 82pp; English.  
 XX New compounds are presented which consist of a cysteine protease  
 CC binding moiety attached by its C-terminal to an oxadiazole, thiadiazole  
 CC or 1,2,4 triazole moiety. These compounds are cysteine protease  
 CC inhibitors useful for inhibiting the enzymatic activity of calpain,  
 CC cathepsin, caspase (e.g. human interleukin-1 beta converting enzyme),  
 CC viral or microbial cysteine protease (e.g. human coronavirus or  
 CC gingipain), or protozoan cysteine protease (e.g. Trypanosoma,  
 CC Schistosoma, Leishmania or Plasmodium protease). They can be used  
 CC e.g. for inhibiting cancer cell growth, tumor progression or tumour  
 CC metastasis, or microbial cell or viral growth (e.g. inhibiting  
 CC hepatitis A virus 3C proteinase, hepatitis C virus endopeptidase 2,  
 CC picornain 3C rhinovirus protease, foot and mouth disease virus 1,  
 CC proteinase, encephalomyelitis virus endopeptidase 2, picornain 2A  
 CC protease), treating allergic response symptoms (e.g. inhibiting  
 CC protease Der p1); treating neurodegenerative disorders (e.g.  
 CC Alzheimer's disease, Parkinson's disease, multiple sclerosis) and  
 CC disorders resulting from ischaemic-reperfusion injury (e.g. stroke,  
 CC myocardial infarction, transplantation, vascular injury or  
 CC cardiovascular collapse or shock); treating inflammatory and  
 CC degenerative diseases (e.g. rheumatoid arthritis, osteoarthritis or  
 CC periodontal disease); or treating pulmonary diseases (e.g. asthma or  
 CC emphysema). They can also be used for detecting or quantifying cysteine  
 CC protease activity in a sample, mixture, biological fluid or tissue; for  
 CC purifying cysteine protease in a sample; or as antibacterial agents,  
 CC herbicides, fungicides or pesticides.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 80.0%; Score 16; DB 20; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 IEP 4  
 Db |||  
 Db 1 IEP 3  
 RESULT 4  
 AAY15640  
 ID AAY15640 standard; Peptide; 4 AA  
 XX  
 AC AAY15640;  
 XX  
 DT 27-JUL-1999 (first entry)  
 DE Peptide used to make fluorescent reporter molecules  
 XX  
 KW Fluorogenic; fluorescent reporter molecule; enzyme substrate;  
 KW apoptosis; protease; peptidase; apoptosis cascade; cancer;  
 KW chemotherapeutic agent; cell death; viral protease activity;  
 XX  
 OS Synthetic.  
 XX  
 PN WO9918956-A1.  
 XX  
 PD 22-APR-1999.  
 XX  
 PF 09-OCT-1998; 98WO-US21231.  
 XX  
 PR 03-MAR-1998; 98US-0033661.  
 XX  
 PP 10-OCT-1997; 97US-0081592

XX (CYTO-) CYTOKIN INC.  
 PA  
 XX Cai SX, Drewe JA, Keana JFW, Weber E, Zhang H;  
 PI WPI; 1999-312448/26.  
 XX  
 DR New fluorogenic or fluorescent reporter molecules  
 PT  
 XX Claim 6, Page 165, 203pp; English.  
 PS  
 XX AAY15618-Y15759 represent peptides used to make the fluorogenic or  
 CC fluorescent reporter molecules of the invention. These molecules  
 CC contain a peptide moiety (e.g. present sequential) which acts as a  
 CC substrate for enzymes involved in apoptosis or protease or peptidase  
 CC enzymes. The compounds can be used as fluorogenic or fluorescent  
 CC substrates for enzymes. Depending on the peptide moiety used, the  
 CC fluorescent molecules can be used for detecting or measuring the  
 CC activity of an enzyme involved in the apoptosis cascade in cells; to  
 CC determine whether a test compound has an effect on an enzyme involved  
 CC in the apoptosis cascade in cells; for determining the sensitivity of  
 CC an animal with cancer to treatment with chemotherapeutic agents or  
 CC determining whether a test substance inhibits, prevents, causes or  
 CC enhances cell death of test cells; for detecting or measuring the  
 CC activity of a viral protease in cells; for determining whether a test  
 CC compound has an effect on the activity of a viral protease in cells;  
 CC and for measuring the activity or determining whether a test substance  
 CC has an effect on the activity of a protease or peptidase in cells.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 70.0%; Score 14; DB 20; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 IEP 4  
 Db |||  
 Db 1 IEP 3  
 RESULT 5  
 AAB28671  
 ID AAB28671 standard; peptide; 4 AA.  
 XX  
 AC AAB28671;  
 XX  
 DT 13-FEB-2001 (first entry)  
 DE Chemotactic peptide pepL.  
 XX  
 KW Chemotactic, osteopontin, vulnery, antiarthritis, antipsoriatic;  
 KW cytostatic; antitumor; antiinflammatory; osteopathic;  
 KW wound healing; cell migration; chemotaxis; atherosclerosis, cancer;  
 KW angiogenic-associated disease; arthritis; psoriasis; haemangioma;  
 KW ocular neovascularisation; cell apoptosis; nitrous oxide production;  
 KW inflammation; osteoporosis; immune disease.  
 XX  
 OS Mammalia.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "N-terminal acetyl"  
 FT  
 XX WO2000063247 A2.  
 PN  
 XX 26-OCT-2000  
 PD  
 XX 17-APP-2000; 2000WO-US10344.  
 PF  
 XX 15-APR-1999; 99US-0129764.  
 PR  
 XX (CHIL) CHILDRENS MEDICAL CENT.

```

XX Ashkar S;
XX WPI: 2000-687159/57.
XX
XX New osteopontin derived chemotactic and inhibitory peptides, useful for
XX promoting scarless wound healing, modulating cellular chemotaxis,
XX treating formation of atherosclerotic plaques and preventing metastasis
XX
XX Claim 17; Page 43; 54pp; English.
XX
XX The present sequence is an osteopontin-derived chemotactic peptide.
XX Such chemotactic peptides are useful for promoting scarless wound
XX healing, modulating chemotaxis and promoting cell migration to a target
XX site in a cell of a subject. They are also used for modulating cellular
XX chemotaxis in a mammalian cell such as smooth muscle cell, a macrophage,
XX an endothelial cell, a vascular cell and a tumorigenic cell. They are
XX useful for treating the formation of atherosclerotic plaques in a
XX subject. The peptides are used for preventing metastasis, treating an
XX angiogenic-associated disease such as arthritis, psoriasis, haemangioma,
XX tumour metastasis or ocular neovascularisation. They are also used for
XX activating cell apoptosis, for modulating nitrous oxide production and
XX for inducing chemotaxis. The peptides are useful for diagnosing, treating
XX and preventing tumour metastasis, inflammation, osteoporosis and immune
XX diseases. They can also be used to enhance an immune response by
XX attracting macrophages.
XX
XX Sequence 4 AA;
XX
XX Query Match 70.0%; Score 14; DB 21; Length 4;
XX Best Local Similarity 50.0%; Pred. No. 7 8e+05;
XX Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 VLDP 4
XX Db 1 MLDP 4
XX
XX RESULT 6
XX AAB22909
XX ID AAB22909 standard; peptide; 4 AA.
XX AC AAB22909;
XX
XX 10-JAN-2001 (first entry)
XX
XX Granzyme B substrate recognition sequence, SEQ ID NO:100.
XX
XX Bioreceptor protein; fusion protein; recognition site;
XX cellular targeting sequence; cellular localisation; fluorescent protein;
XX protease activity detection; toxin detection; cellular stress detection;
XX drug discovery; cell based screening; protease recognition site;
XX cleavage site.
XX
XX Unidentified.
XX
XX WQ2000050872-A2
XX
XX 31-AUG-2000
XX
XX 25 FEB 2000, 2000WO USC4794.
XX
XX 26-FEB-1999; 90US 0122152.
XX 08-MAP-1999; 90US-0123399.
XX 12-JUL-1999; 90US 0352171
XX
XX (CELL-1) CELLULINICS INC.
XX
XX Giuliano KA, Kapur R;
XX
XX WPI: 2000-594086/56.
XX N-ESDB; ABA0240c

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XX Automated cell-based characterization of toxin by contacting cells
XX containing luminescent reporter molecules with test substance and
XX analyzing optically
XX
XX Example 11, Fig 20B; 336pp; English.
XX
XX The invention relates to systems, methods and reagents for cell-based
XX screening or detection of compounds which affect particular biological
XX functions. The methods of the invention utilise fluorescent bioreceptor
XX molecules which, when acted on by a compound of interest, cause an
XX alteration in the cellular distribution of at least the fluorescent
XX moiety. In one embodiment, the biosensors comprise heat shock proteins
XX (HSPs) fused to a fluorescent protein (e.g., jellyfish green fluorescent
XX protein (GFP), or derivatives thereof). Such biosensors are located in
XX the cytoplasm, but on stress activation translocate to the nucleus. In
XX another embodiment bioreceptor proteins can be used to detect protease
XX activity. Such protease bioreceptor fusion proteins comprise one or more
XX fluorescent proteins; a recognition signal which is cleaved by the
XX protease; and at least one cellular localisation signal. The latter two
XX components may be components of a single protein which is acted upon by
XX the protease, or may be from heterologous sources. Due to the
XX localisation signal, the bioreceptor protein is localised to a
XX particular region of the cell. Once acted on by the protease of interest,
XX the fluorescent protein is cleaved from the localisation sequence, and
XX is free to migrate to other locations within the cell. The presence of a
XX second localisation signal attached to the fluorescent protein enables
XX the fluorescent protein to be directed to a different cellular
XX compartment after cleavage of the protease recognition sequence. The
XX change in distribution of the fluorescent protein can be detected using
XX imaging methods with a high degree of spatial resolution. The methods
XX and biosensors of the invention can be used to investigate a wide range
XX of cellular activities and to screen compounds which modulate these
XX activities. Biosensors containing a recognition site for caspase, for
XX example, may be used for the screening of compounds which modulate
XX apoptosis, while biosensors containing other protease recognition sites
XX may be used for the detection of proteolytic toxins (such as anthrax
XX lethal factor). The method provides improved target validation and
XX candidate compound optimisation by combining many cell screening formats
XX with fluorescence-based molecular reagents and computer-based feature
XX extraction, data analysis and automation, resulting in increased
XX quantity and speed of data collection and faster evaluation of drug
XX candidates. Sequences AAB22886-92220 and AAB22935 represent protease
XX recognition sites which may be used as components of biosensor fusion
XX proteins of the invention.
XX
XX Sequence 4 AA;
XX
XX Query Match 70.0%; Score 14; DB 21; Length 4;
XX Best Local Similarity 66.7%; Pred. No. 7 8e+05;
XX Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 LEP 4
XX Db 1 IEP 3
XX
XX RESULT 7
XX AAY79611
XX ID AAY79611 standard; peptide; 4 AA
XX AC AAY79611;
XX
XX 20-AUG-2000 (first entry)
XX
XX Granzyme-B substrate recognition sequence.
XX
XX protease; biosensor; granzyme-B; substrate recognition sequence;
XX cell screening; assay; analysis; drug discovery.
XX
XX Unidentified.
XX
XX WQ200006408 A2

```

XX 11-MAY-2000  
 XX 29-OCT-1999; 99WO-US26431  
 XX 30-OCT-1998; 98US-0106308  
 XX 26-MAY-1999; 99US-0136078  
 XX (CELL-) CELLONICS INC.  
 PI Giuliano KA, Bright G, Olsen K, Burroughs Tencza S;  
 DR WPI, 2000-365644/31.  
 DR N PDB; AAA27600.  
 XX Recombinant nucleic acid encoding a protease biosensor useful for  
 PT fluorescence based cell and molecular biochemical assays for drug  
 PT discovery comprising three operably linked nucleic acid sequences  
 XX Claim 15; Fig 20B; 218pp; English.  
 XX The present sequence is that of a granzyme-B substrate  
 CC recognition sequence, which can be included in novel recombinant  
 CC protease biosensors (pbe) of the invention. The pbe (see AAY70621-64)  
 CC comprise a first domain (see AAY70621-67) comprising at least 1  
 CC detectable polypeptide signal, a second domain (see AAY70621-67)  
 CC comprising at least 1 protease recognition site, such as the  
 CC present sequence; and a third domain (see AAY70621-37) comprising at  
 CC least 1 reactant target sequence. A recombinant nucleic acid (see  
 CC AAY70627-41) encoding the pbe, an expression vector, and a genetically  
 CC engineered host cell are also claimed. A claimed method for  
 CC identifying compounds that modify protease activity in a cell  
 CC involves contacting a host cell that possesses the recombinant pbe  
 CC with a test compound, and determining the pbe distribution in the  
 CC host cell, where changes in the distribution of the pbe are  
 CC correlated with modification of protease activity by the test  
 CC compound. Claimed kits for identifying compounds that modify  
 CC protease activity in a host cell include the recombinant nucleic  
 CC acid, or the recombinant pbe, or the vector, or the host cell. The  
 CC pbe is useful in high content screens to detect in vivo activation  
 CC of enzymatic activity, and to identify specific activity based on  
 CC cleavage of a known recognition motif.  
 XX Sequence 4 AA;  
 SQ Query Match 70.0%; Score 14; DB 21; Length 4;  
 Best Local Similarity 66.7%; Pred No 7.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LEP 4  
 Db :||  
 1 IEP 3  
 RESULT 8  
 AAY80804  
 ID AAY80804 standard; peptide; 4 AA.  
 XX AAY80804;  
 AC AAY80804;  
 DT 22-MAY-2000 (first entry)  
 XX Fluorophore-labelled granzyme B substrate peptide, SEQ ID NO:21.  
 DE protease substrate; fluorescent label; fluorophore; rhodamine.  
 KW blocking group; halobenzoyl group; cleavage; caspase; viral protease;  
 PW methionine aminopeptidase type 2, MetAP 2, drug screening.  
 XX Synthetic.  
 OS WO200004914-A1.  
 XX 03-FEB-2000.  
 XX 03-APR-2000; 2000JP-0105410.

XX 21-JUL-1999; 99WO-US16423.  
 XX 21-JUL-1998; 98US-0807642.  
 XX (CYTO-) CYTOVIA INC.  
 PA (ZHAN/) ZHANG H.  
 PA (CAIS/) CAI S X.  
 PA (DREW/) DREW J A.  
 PA (YANG/) YANG W.  
 PI Zhang H, Cai SX, Drewe JA, Yang W;  
 DR WPI, 2000-195079/17.  
 XX New fluorescently labeled amino acids or peptides, used as substrates  
 PT for detecting enzymes or their modulators, e.g. anticancer or antiviral  
 PT agents, contains a halobenzoyl N blocking group.  
 XX Claim 3; Page 100; 174pp; English.  
 XX The invention relates to fluorescently labelled peptides containing  
 CC a halobenzoyl group on the fluorophore. They are of the structure  
 CC peptide-Y-Z, where Y represents a halo substituted benzoyl blocking  
 CC group, Z is a fluorescent or fluorogenic moiety (preferably a  
 CC fluorophore), and the peptide Y-Z is cleavable by the enzyme being  
 CC assayed. The labelled peptides are reporters for detecting intracellular  
 CC proteolytic enzymes, particularly caspases and other enzymes involved in  
 CC apoptosis; viral proteases (e.g., HIV, herpes simplex virus 1, human  
 CC cytomegalovirus and hepatitis C virus proteases); and methionine  
 CC aminopeptidase type 2 (MetAP 2). The peptides are particularly useful to  
 CC identify modulators of these enzymes which may be potentially useful as  
 CC agents for treating conditions such as cancer, neurodegeneration,  
 CC autoimmune diseases, myocardial infarction and viral infection.  
 CC Modulators identified may also be used to prolong the life of cells being  
 CC cultured with recombinant protein production, or to monitor the treatment  
 CC of cancer with chemotherapeutic agents. Inhibitors of MetAP 2 are  
 CC potential anti-angiogenic or anticancer agents. Sequences  
 CC AAY80804 represent peptides, some of which are specifically  
 XX claimed, which may be used in assay methods according to the invention.  
 XX Sequence 4 AA;  
 SQ Query Match 70.0%; Score 14; DB 21; Length 4;  
 Best Local Similarity 66.7%; Pred No 7.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LEP 4  
 Db :||  
 1 IEP 3  
 RESULT 9  
 AAU79766  
 ID AAU79766 standard; peptide; 4 AA.  
 XX AAU79766;  
 AC AAU79766;  
 DT 30-JUL-2002 (first entry)  
 XX Chicken bone derived peptide #1, useful as ACE inhibitor.  
 DE Angiotensin converting enzyme inhibitor; ACEI; health food;  
 PW food additive; pharmaceutical product; lowering blood pressure;  
 KW hypertension; chicken essence by-product; chicken bone.  
 XX Gallus sp.  
 OS JP2001163496-A  
 XX 19-JUN-2001.  
 XX 03-APR-2000; 2000JP-0105410.

XX 01-DEC-1999; 99TW-0120997.  
 XX (FOOD-) FOOD INC RES & DEV INST.  
 XX WPI; 2001-574451/65.  
 XX New peptides capable of inhibiting angiotensin converting enzyme for  
 PT use in pharmaceutical compositions, in health foods and as food  
 FT additives -  
 XX  
 XX Claim 1, Page 2; 39pp; Japanese.  
 XX The present invention relates to novel peptides having angiotensin  
 CC converting enzyme (ACE) inhibitory activity. Also described are  
 CC methods for preparing products having ACE inhibitory activity, a  
 CC pharmaceutical composition for use in the inhibition of ACE, and  
 CC a health food or a food additive for use in the inhibition of  
 CC ACE. The peptides of the invention are useful as ACE inhibitors (ACEI).  
 CC They are useful in pharmaceutical products and health foods, and as  
 CC food additives. Such compositions may be used for lowering blood pressure  
 CC and creating hypertension. The manufacturing cost of the peptides of the  
 CC invention is considerably less than prior art as the peptide can be  
 CC produced from waste materials. Also the values of chicken essence  
 CC by products can be improved. The present peptide derived from chicken  
 CC bone is useful as an ACE inhibitor.  
 XX  
 XX Sequence 4 AA;  
 SQ  
 Query Match 70.0%; Score 14; DB 22; Length 4;  
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 VLPP 4  
 DB 1 VLPP 4  
 RESULT 10  
 ID AAB82937 standard; Peptide; 4 AA.  
 XX AAB82937;  
 AC AAB82937;  
 XX 21-DEC-2001 (first entry)  
 DT Granzyme B peptide substrate.  
 DE Granzyme B; caspase, predru3; therapy; ACEFT; cancer, tumour;  
 KW inflammation; infection.  
 FW Synthetic.  
 OS  
 XX W200012400 AC  
 PN 10-AUG-2001.  
 XX 22 FEB 2001, 2001WO 080000  
 PF 24-FEB-2000, 2000US 194170P.  
 PR (GETH ) GENENTECH INC.  
 XX Carter PJ, Gazzard L;  
 PI WPI; 2001 611217/70.  
 XX Delivering active agents to cell-types of interest for therapeutic  
 PT purposes, comprises administering a cell-type targeted caspase  
 PT conjugate and a pro-agent which is converted to the active agent in the  
 PT presence of the caspase -  
 XX Disclosure; Page 13; 61pp; English.

XX The present sequence is that of the preferred peptide substrate  
 CC of granzyme-B. The invention provides methods for the localised  
 CC delivery of pharmaceutical agents by the administration of a  
 CC caspase conjugate that targets a cell type of interest and the  
 CC additional administration of a pro-agent, which is locally  
 CC converted by the caspase to an active agent. In preferred  
 CC embodiments the targeting component is an antibody, the drug is  
 CC preferably a cytotoxic or chemotherapeutic agent, and the  
 CC prodrug moiety comprises a caspase-cleavable peptide, especially  
 CC a group II caspase cleavable peptide (see AAB82926), which is a  
 CC very poor substrate for granzyme B and for proinflammatory  
 CC caspases. The methods allow treatment of diseases or disorders  
 CC characterised by the appearance or presence of a particular cell  
 CC type. Such cells include bacterially and virally infected cells  
 CC expressing cell surface epitopes characteristic of the infection,  
 CC neoplastic and malignant cells such as tumour cells, and cells  
 CC characterised by their presence or appearance in areas of  
 CC inflammation.  
 XX  
 XX Sequence 4 AA;  
 SQ  
 Query Match 70.0%; Score 14; DB 22; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LEP 4  
 DB 1 LEP 3  
 RESULT 11  
 ID AAG62561 standard; peptide; 4 AA.  
 XX AAG62561;  
 AC AAG62561;  
 XX 05-SEP-2001 (first entry)  
 DT Cresyl violet substituted caspase inhibitor substrate SEQ ID NO: 16.  
 DE Cresyl violet substituted caspase inhibitor substrate;  
 KW Caspase inhibitor substrate; cresyl violet; fluorogenic substrate;  
 FW metastasis; cancer; protease.  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FT Modified-site 1 /label= CTHPP  
 FT /note= "optionally modified by carboxybenzoxy or acetyl"  
 XX US6235493-B1.  
 PN 22-MAY-2001  
 PF 05-AUG-1998; 98US-0130193.  
 XX 06-AUG-1997; 97US 0056392.  
 PF (FEB ) UNIV CALIFORNIA.  
 XX Bissell ER, Smith RF;  
 PI WPI; 2001-431695/46.  
 XX Method for detection of an enzyme in vivo or in vitro in a cell using  
 PT an amino acid-substituted cresyl violet fluorogenic substrate -  
 XX Claim 6; Column 32; 27pp; English.  
 XX The present invention describes a method of detecting the presence of an  
 CC enzyme in living cells, involving contacting the cell with an amino acid  
 CC substituted cresyl violet fluorogenic substrate and quantifying the

CC fluorescence produced. This is particularly useful for detecting enzymes  
 CC such as proteases and caspases, which may be linked to cancer metastasis.  
 CC The present sequence is a caspase inhibitor substrate used in the  
 CC exemplification of the invention

XX SQ Sequence 4 AA;  
 Query Match 70.0%; Score 14; DB 22; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LEP 4  
 Db 1 IEP 3

RESULT 12  
 AAR29759  
 ID AAR29759 standard; peptide; 4 AA.  
 AC AAR29759;  
 XX  
 DT 28 FEB-2001 (first entry)  
 XX  
 DE Escherichia coli ribosomal protein L16 N-terminus.  
 XX  
 KW Recombinant human haemoglobin, rHuH1.1, bacterial expression,  
 KW N-terminal methionine methylation signal; demethylation;  
 KW Escherichia coli; non-immunogenic; pharmaceutical composition.  
 XX  
 OS Escherichia coli.  
 XX  
 PN US6140071-A.  
 XX  
 PD 31-OCT-2000.  
 XX  
 PF 27 JAN-1994; 94US-0188374.  
 XX  
 PR 27 JAN 1994, 94US-0188374.  
 XX  
 PA (SOMA-) SOMATOGEN INC.  
 XX

PI Aitken JF, Apostol IZ, Levine JD, Lippincott JA;  
 XX

DR WPI: 2001-044457/06.  
 XX

PT Decreasing methylation of an N-terminus protein, especially hemoglobin  
 PT having proline at amino acid position 4, useful for producing  
 PT demethylated proteins for treating diseases, by altering this amino  
 PT acid to a non-proline residue

XX PS Disclosure; Column 1; 26pp; English.  
 XX

CC The invention relates to a method of decreasing the amount of N-terminal  
 CC methionine methylation on a protein expressed in a bacterium. The  
 CC bacterial methyltransferase which directs N-terminal methionine  
 CC methylation recognises proteins which have a proline residue at position  
 CC 4 (e.g., the bacterial ribosomal protein L16 and the bacterial chemotaxis  
 CC protein CheZ). The method comprises introducing mutations into the DNA  
 CC encoding the protein so that residue 4 is a non-proline residue, thereby  
 CC reducing the degree of N-terminal methylation when the protein is  
 CC expressed in a bacterium. The method is useful for decreasing methylation  
 CC of a protein, particularly a recombinantly produced protein. The  
 CC demethylated protein can be used in a pharmaceutical composition for  
 CC the treatment of a disease but with less likelihood of eliciting an  
 CC immunological response. These demethylated proteins may be used as  
 CC therapeutic agents for the treatment and/or amelioration of disease or  
 CC symptoms associated with a disease. The exemplifications describe  
 CC the expression of a recombinant human haemoglobin construct (rHuH1.1) in  
 CC Escherichia coli, and its modification such that residue 4 of the  
 CC di-alpha chain of the recombinant haemoglobin is altered from proline  
 CC to a non-proline residue. The present sequence represents a peptide  
 CC referred to in the disclosure of the invention.

XX SQ Sequence 4 AA;  
 Query Match 70.0%; Score 14; DB 22; Length 4;  
 Best Local Similarity 50.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLEP 4  
 Db 1 MLQP 4

RESULT 13  
 AAE19128  
 ID AAE19128 standard; peptide; 4 AA.  
 XX  
 AC AAE19128;  
 XX

DT 21 MAY 2002 (first entry)  
 XX

DE Granzyme B peptide.  
 XX

KW Luciferase; enzyme; protease; cell growth; apoptosis; therapeutic;  
 KW cell death; granzyme B.  
 XX

OS Unidentified.  
 XX

PN WO2000306458-A2.  
 XX

PD 24 JAN-2002.  
 XX

PF 17-JUL-2001; 2001WO-US22478.  
 XX

PP 19-JUL-2000; 2000US-0619047.  
 XX

PA (CHEM-) CHEMICON INT INC.  
 XX

PI Leng J;  
 XX

DR WPI: 2002-195809/25.  
 XX

PT New purified luciferase polypeptide, useful for identifying protease  
 PT activity modulators, comprises recognition site cleavable by protease,  
 PT where cleavage of polypeptide results in decreased luciferase activity  
 PT

XX PS Claim 63; Page 25; 56pp; English.  
 XX

CC The invention relates to a purified polypeptide having luciferase  
 CC activity and a recognition site specifically cleavable by a protease,  
 CC where cleavage results in a decrease in luciferase activity. The  
 CC polypeptide comprises a localisation sequence which is linked to the  
 CC luciferase polypeptide by the cleavable recognition sequence. The  
 CC polypeptide is useful for identifying a protease (caspase) activity  
 CC modulator, an inhibitor of apoptosis and for detecting luciferase  
 CC activity in a sample. The polypeptide is used for characterising and  
 CC identifying cellular processes associated with metabolism, cell growth  
 CC and cell death e.g. apoptosis and for measuring protease activity. The  
 CC protease measurement methods are useful for characterising, identifying  
 CC cellular biochemical pathways as well as identifying diagnostic and  
 CC agents for modulating diseases or disorders associated with  
 CC biochemical pathways. The polypeptide is also useful as a substrate to  
 CC study agents or conditions that cleave the recognition site and for  
 CC determining amount of protease in a sample and for monitoring the  
 CC activity of protease inside a cell that expresses a recombinant  
 CC luciferase. The present sequence is granzyme B peptide used in the  
 CC invention.

XX SQ Sequence 4 AA;  
 Query Match 70.0%; Score 14; DB 23; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4  
:||  
Db 1 IEP 3

## RESULT 14

AAM50406  
ID AAM50406 standard; Peptide; 4 AA.

XX  
AC AAM50406;  
XX

DT 12-MAR-2002 (first entry)  
XX

DE Tumour associated activatable guarding moiety.  
XX

XX Magnetic resonance imaging; MRI; cancer; detection;  
KW contrasting agent; tumour associated activatable guarding moiety;  
KW TAAGM.  
XX

OS Synthetic.  
XX

XX Key  
FH Location/Qualifiers  
FT Modified-site 1  
FT /note= "N-terminal acetyl"  
FT Modified-site 4  
FT /note= "C-terminal aminomethylcoumarin"  
FT  
XX  
PN WO200182976-A2.  
XX  
PD 08-NOV-2001.  
XX  
XX 04-MAY-2001; 2001WO-US14470.  
XX  
PF  
XX 04-MAY-2001; 2000US-201816P.  
PF  
XX 17-NOV-2000; 2000US-0715859.  
XX  
XX (PSE ) RESEARCH CORP TECHNOLOGIES INC.  
XX  
XX Meade TJ;  
XX  
XX WPI; 2002-075134/10.  
XX  
XX New magnetic resonance imaging contrast agents for detection of  
PT cancerous cells and tissues -  
XX  
XX Disclosure, Page 27, 61pp; English.  
XX

CC The present peptide is an example of a tumour associated activatable  
CC guarding moiety (TAAGM) that is used in a preferred embodiment of  
CC the invention. A claimed magnetic resonance imaging (MRI) contrast  
CC agent composition comprises: a gadolinium (III) ion bound to a first  
CC chelator such that the ion has coordination atoms in at least 7 of  
CC its coordination sites; and a TAAGM covalently attached to the first  
CC chelator which hinders the rapid exchange of water in the remaining  
CC coordination sites of the Gd(III) ion. The novel MRI contrast  
CC agents can target substances that are associated with cancer. By  
CC using a targeting moiety, the MRI agents become more effective,  
CC discriminatory and selective with regard to signal detection of  
CC disease pathology.  
XX  
SQ Sequence 4 AA;  
Query Match 70.0%; Score 14; DB 23; Length 4;  
Best Local Similarity 66.7%; Pred. No. 7.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4  
:||  
Db 1 IEP 3

## RESULT 15

AAM50466  
ID AAM50466 standard; Peptide; 4 AA.

XX  
AC AAM50466;  
XX

DT 12-MAR-2002 (first entry)  
XX

DE Tumour associated activatable guarding moiety.  
XX

XX Magnetic resonance imaging; MRI; cancer; detection;  
KW contrasting agent; tumour associated activatable guarding moiety;  
KW TAAGM.  
XX

OS Synthetic.  
XX

XX Key  
FH Location/Qualifiers  
FT Modified-site 1  
FT /note= "N-terminal acetyl"  
FT Modified-site 4  
FT /note= "C-terminal pNA"  
FT  
XX  
PN WO200182976-A2.  
XX  
PD 08-NOV-2001.  
XX  
XX 04-MAY-2001; 2001WO-US14470.  
XX  
PF  
XX 04-MAY-2001; 2000US-201816P.  
PF  
XX 17-NOV-2000; 2000US-0715859.  
XX  
XX (PSE ) RESEARCH CORP TECHNOLOGIES INC.  
XX  
XX Meade TJ;  
XX  
XX WPI; 2002-075134/10.  
XX  
XX New magnetic resonance imaging contrast agents for detection of  
PT cancerous cells and tissues -  
XX  
XX Disclosure, Page 27, 61pp; English.  
XX

CC The present peptide is an example of a tumour associated activatable  
CC guarding moiety (TAAGM) that is used in a preferred embodiment of  
CC the invention. A claimed magnetic resonance imaging (MRI) contrast  
CC agent composition comprises: a gadolinium (III) ion bound to a first  
CC chelator such that the ion has coordination atoms in at least 7 of  
CC its coordination sites; and a TAAGM covalently attached to the first  
CC chelator which hinders the rapid exchange of water in the remaining  
CC coordination sites of the Gd(III) ion. The novel MRI contrast  
CC agents can target substances that are associated with cancer. By  
CC using a targeting moiety, the MRI agents become more effective,  
CC discriminatory and selective with regard to signal detection of  
CC disease pathology.  
XX  
SQ Sequence 4 AA;  
Query Match 70.0%; Score 14; DB 23; Length 4;  
Best Local Similarity 66.7%; Pred. No. 7.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

AAM50407  
ID AAM50407 standard; Peptide; 4 AA.

XX  
AC AAM50407;  
XX

DT 12-MAR-2002 (first entry)  
XX

DE Tumour associated activatable guarding moiety.  
XX

XX Magnetic resonance imaging; MRI; cancer; detection;  
KW contrasting agent; tumour associated activatable guarding moiety;  
KW TAAGM.  
XX

OS Synthetic.  
XX

XX Key  
FH Location/Qualifiers  
FT Modified-site 1  
FT /note= "N-terminal acetyl"  
FT Modified-site 4  
FT /note= "C-terminal pNA"  
FT  
XX  
PN WO200182976-A2.  
XX  
PD 08-NOV-2001.  
XX  
XX 04-MAY-2001; 2001WO-US14470.  
XX  
PF  
XX 04-MAY-2001; 2000US-201816P.  
PF  
XX 17-NOV-2000; 2000US-0715859.  
XX  
XX (PSE ) RESEARCH CORP TECHNOLOGIES INC.  
XX  
XX Meade TJ;  
XX  
XX WPI; 2002-075134/10.  
XX  
XX New magnetic resonance imaging contrast agents for detection of  
PT cancerous cells and tissues -  
XX  
XX Disclosure, Page 27, 61pp; English.  
XX

CC The present peptide is an example of a tumour associated activatable  
CC guarding moiety (TAAGM) that is used in a preferred embodiment of  
CC the invention. A claimed magnetic resonance imaging (MRI) contrast  
CC agent composition comprises: a gadolinium (III) ion bound to a first  
CC chelator such that the ion has coordination atoms in at least 7 of  
CC its coordination sites; and a TAAGM covalently attached to the first  
CC chelator which hinders the rapid exchange of water in the remaining  
CC coordination sites of the Gd(III) ion. The novel MRI contrast  
CC agents can target substances that are associated with cancer. By  
CC using a targeting moiety, the MRI agents become more effective,  
CC discriminatory and selective with regard to signal detection of  
CC disease pathology.  
XX  
SQ Sequence 4 AA;  
Query Match 70.0%; Score 14; DB 23; Length 4;  
Best Local Similarity 66.7%; Pred. No. 7.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4  
:||  
Db 1 IEP 3

## RESULT 16

AAM50466  
ID AAM50466 standard; Peptide; 4 AA.

XX  
AC AAM50466;  
XX

DT 12-MAR-2002 (first entry)  
XX

DE Tumour associated activatable guarding moiety.  
XX

XX Magnetic resonance imaging; MRI; cancer; detection;  
KW contrasting agent; tumour associated activatable guarding moiety;  
KW TAAGM.  
XX

OS Synthetic.  
XX

XX Key  
FH Location/Qualifiers  
FT Modified-site 1  
FT /note= "N-terminal acetyl"  
FT Modified-site 4  
FT /note= "C-terminal pNA"  
FT  
XX  
PN WO200182976-A2.  
XX  
PD 08-NOV-2001.  
XX  
XX 04-MAY-2001; 2001WO-US14470.  
XX  
PF  
XX 04-MAY-2001; 2000US-201816P.  
PF  
XX 17-NOV-2000; 2000US-0715859.  
XX  
XX (PSE ) RESEARCH CORP TECHNOLOGIES INC.  
XX  
XX Meade TJ;  
XX  
XX WPI; 2002-075134/10.  
XX  
XX New magnetic resonance imaging contrast agents for detection of  
PT cancerous cells and tissues -  
XX  
XX Disclosure, Page 27, 61pp; English.  
XX

CC The present peptide is an example of a tumour associated activatable  
CC guarding moiety (TAAGM) that is used in a preferred embodiment of  
CC the invention. A claimed magnetic resonance imaging (MRI) contrast  
CC agent composition comprises: a gadolinium (III) ion bound to a first  
CC chelator such that the ion has coordination atoms in at least 7 of  
CC its coordination sites; and a TAAGM covalently attached to the first  
CC chelator which hinders the rapid exchange of water in the remaining  
CC coordination sites of the Gd(III) ion. The novel MRI contrast  
CC agents can target substances that are associated with cancer. By  
CC using a targeting moiety, the MRI agents become more effective,  
CC discriminatory and selective with regard to signal detection of  
CC disease pathology.  
XX  
SQ Sequence 4 AA;  
Query Match 70.0%; Score 14; DB 23; Length 4;  
Best Local Similarity 66.7%; Pred. No. 7.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4  
:||  
Db 1 IEP 3

DE Tumour associated activatable guarding moiety.

XX Magnetic resonance imaging; MRI; cancer, detection,  
 KW contrasting agent; tumour associated activatable guarding moiety,  
 KW TAAGM.

XX Synthetic.

OS Key  
 FH Modified-site 1 Location/Qualifiers  
 FT /note= "N-terminal acetyl"

FT Modified-site 4  
 FT /note= "C-terminal aldehyde (pseudo acid)"

XX WO200182976-A2

PN 08 NOV 2001

XX 04-MAY-2001; 2001WO-US14470.

XX 04-MAY-2000; 2000US-201816P

PR 17-NOV-2000; 2000US-0715859.

XX (RESE ) RESEARCH CORP TECHNOLOGIES INC.

PA Meade TJ;

PI WPI; 2002-075134/10.

XX New magnetic resonance imaging contrast agents for detection of  
 PT cancerous cells and tissues

XX Disclosure; Page 29; 61pp; English.

PS The present peptide is an example of a tumour associated activatable  
 CC guarding moiety (TAAGM) that is used in a preferred embodiment of  
 CC the invention. A claimed magnetic resonance imaging (MRI) contrast  
 CC agent composition comprises a gadolinium (III) ion bound to a first  
 CC chelator such that the ion has coordination atoms in at least 7 of  
 CC its coordination sites; and a TAAGM covalently attached to the first  
 CC chelator which hinders the rapid exchange of water in the remaining  
 CC coordination sites of the Gd(III) ion. The novel MRI contrast  
 CC agents can target substances that are associated with cancer. By  
 CC using a targeting moiety, the MRI agents become more effective,  
 CC discriminatory and selective with regard to signal detection of  
 CC disease pathology.

XX Sequence 4 AA;

SQ Query Match 70.0%; Score 14; DB 23; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4  
 Db :|||  
 1 IEP 3

RESULT 17  
 AAM50470  
 ID AAM50470 standard; Peptide; 4 AA.  
 XX AAM50470;  
 AC AAM50470;  
 XX 12-MAR-2002 (first entry)  
 DT Tumour associated activatable guarding moiety.  
 DE Magnetic resonance imaging; MRI; cancer, detection;  
 KW contrasting agent; tumour associated activatable guarding moiety,  
 KW TAAGM.  
 XX Synthetic.

XX Key  
 FH Modified-site 1 Location/Qualifiers  
 FT /note= "N-terminal acetyl"

FT Modified-site 4  
 FT /note= "C-terminal aminomethyl coumarin"

XX WO200182976-A2

PN 08-NOV-2001.

XX 04 MAY 2001; 2001WO-US14470

XX 04-MAY-2000; 2000US-201816P

PR 17-NOV-2000; 2000US-0715859.

XX (RESE ) RESEARCH CORP TECHNOLOGIES INC.

PA Meade TJ;

PI WPI; 2002-075134/10.

XX New magnetic resonance imaging contrast agents for detection of  
 PT cancerous cells and tissues

XX Disclosure; Page 28; 61pp; English.

PS The present peptide is an example of a tumour associated activatable  
 CC guarding moiety (TAAGM) that is used in a preferred embodiment of  
 CC the invention. A claimed magnetic resonance imaging (MRI) contrast  
 CC agent composition comprises a gadolinium (III) ion bound to a first  
 CC chelator such that the ion has coordination atoms in at least 7 of  
 CC its coordination sites; and a TAAGM covalently attached to the first  
 CC chelator which hinders the rapid exchange of water in the remaining  
 CC coordination sites of the Gd(III) ion. The novel MRI contrast  
 CC agents can target substances that are associated with cancer. By  
 CC using a targeting moiety, the MRI agents become more effective,  
 CC discriminatory and selective with regard to signal detection of  
 CC disease pathology.

XX Sequence 4 AA;

SQ Query Match 70.0%; Score 14; DB 23; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4  
 Db :|||  
 1 IEP 3

RESULT 18  
 AAM50471  
 ID AAM50471 standard; Peptide; 4 AA.  
 XX AAM50471;  
 AC AAM50471;  
 XX 12-MAR-2002 (first entry)  
 DT Tumour associated activatable guarding moiety.  
 DE Magnetic resonance imaging; MRI; cancer, detection;  
 KW contrasting agent; tumour associated activatable guarding moiety,  
 KW TAAGM.  
 XX Synthetic.

OS Key  
 FH Modified-site 1 Location/Qualifiers  
 FT /note= "N-terminal acetyl"

FT Modified-site 4  
 FT /note= "C-terminal pNA"

XX

PN WC200102976-A2.  
 XX 08-NOV-2001.  
 XX 04-MAY-2001, 2001W9-0514430  
 XX 04-MAY-2000, 2000US-201816P  
 PF 17-NOV-2000, 2000US-0715859.  
 XX (PSE ) RESEARCH CORP TECHNOLOGIES INC.  
 PA Meade TJ;  
 XX WPI; 2002-075114/10.  
 XX New magnetic resonance imaging contrast agents for detection of  
 PT cancerous cells and tissues -  
 XX Disclosure; Page 28; 61pp; English.  
 XX The present peptide is an example of a tumour associated activatable  
 CC guarding moiety (TAAGM) that is used in a preferred embodiment of  
 CC the invention. A claimed magnetic resonance imaging (MRI) contrast  
 CC agent composition comprises: a gadolinium (III) ion bound to a first  
 CC chelator such that the ion has coordination atoms in at least 7 of  
 CC its coordination sites, and a TAAGM covalently attached to the first  
 CC chelator which hinders the rapid exchange of water in the remaining  
 CC coordination sites of the Gd(III) ion. The novel MRI contrast  
 CC agents can target substances that are associated with cancer. By  
 CC using a targeting moiety, the MRI agents become more effective,  
 CC discriminatory and selective with regard to signal detection of  
 CC disease pathology.  
 XX Sequence 4 AA;  
 SQ Query Match 70.0%; Score 14; DB 23; Length 4;  
 Best Local Similarity 66.7%; Pred No 7 Re+05;  
 Matches 2, Conservative 1; Mismatches 0, Indels 0, Gaps 0;  
 QY 2 LEP 4  
 Db 1 IEP 3  
 RESULT 19  
 AAP71434  
 XX AAP71434 standard; Protein; 4 AA.  
 AC AAP71434;  
 XX 03-MAY-1991 (first entry)  
 DT Immunomodulator peptide #10 inhibits HIV-T4 interaction.  
 XX AIDS; T4 cell receptor; immunomodulation.  
 KW Synthetic.  
 XX WO8703601-A.  
 XX 18-JUN-1987.  
 XX 08-DEC-1986; 86WO-4002717.  
 XX 08-DEC-1985, 85FR-0018155.  
 XX (INSP ) INST PASTEUR.  
 PA (AUFRI/) AUFRAY C.  
 XX Auffray C, Montagnier L, Klatzmann D, Charron D;  
 XX WPI; 1987-177935/25.  
 XX

PT New peptide derivs. contg. specified exposed tetra-peptide  
 PT sequences - inhibiting interaction of AIDS virus with T4 cell  
 PT receptors  
 XX Claim 18; Page 50; 57pp; French.  
 XX The tetrapeptide corresponds to the conserved sequence immediately  
 CC preceding the RPS peptide motif of the Type II HLA antigens of  
 CC HTLVIII, ARV2, LAV1a and LV. It is used to provoke production of  
 CC monoclonal antibodies specific to the peptide.  
 CC See also AAP71422-P71433 and AAP71435-7.  
 XX Sequence 4 AA;  
 SQ Query Match 65.0%; Score 13; DB 8; Length 4;  
 Best Local Similarity 100.0%; Pred No 7.8e+05;  
 Matches 3, Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VLE 3  
 Db 1 VLE 3  
 RESULT 20  
 AAP23726  
 ID AAP23726 standard; peptide, 4 AA.  
 XX AAP23726,  
 AC AAP23726,  
 XX 26-OCT-1992 (first entry)  
 DT ACE inhibitor peptide.  
 XX ACE inhibitor peptide.  
 DE Angiotensin converting enzyme; vasodepression.  
 KW Synthetic.  
 XX JP04091097-A  
 XX 24-MAR-1992.  
 XX 03-AUG-1990; 90JP-0205000.  
 XX 03-AUG-1990; 90JP-0205000.  
 XX (NISS ) NISSHIN FLOUR MILL KK.  
 XX WPI; 1992-148004/18.  
 XX New peptide as ACE inhibitor - with vasodepressive and  
 PT vasopressive inhibiting activity  
 XX Claim 1; Page 1; 7pp; Japanese.  
 XX By admin. of a very small amt. of the ACE inhibitor, vasodepressor  
 CC activity and vasopressor inhibiting activity can be obtd. Also, as it  
 CC is a white water soluble powder, it can be administered directly or as  
 CC an aq. soln, orally or parenterally. It can be prepd. easily by  
 CC simple chemical synthesis.  
 XX Sequence 4 AA;  
 SQ Query Match 65.0%; Score 13; DB 13; Length 4;  
 Best Local Similarity 66.7%; Pred No 7.8e+05;  
 Matches 2, Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LEP 4  
 Db 1 LQP 3  
 RESULT 21  
 AA093983



ID AAW93983 standard; peptide; 4 AA.  
 AC AAW93983;  
 XX  
 DT 01-JUL-1999 (first entry)  
 XX  
 DE Antineoplastic peptide 4.  
 XX  
 KW Tetrapeptide; tumour; delactarin; antineoplastic activity; lung, breast,  
 KW intestine; bladder; rectum; uterus; prostate; leukaemia; lymphoma;  
 KW neoplastic disease.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 1 /note= "Me2-Val"  
 FT Modified-site 3 /note= "Me-Val"  
 FT Modified-site 4 /note= "Pro-OMe"  
 FT  
 FT  
 FT  
 FT  
 FT  
 PN DE4415998-A1.  
 XX  
 XX 09 NOV-1995.  
 PD  
 XX 06 MAY-1994; 94DE-4415998.  
 PF  
 XX  
 PR 06 MAY-1994; 94DE-4415998.  
 XX  
 XX (BADI ) BASF AG.  
 XX  
 XX Amberg W, Bernard H, Buschmann E, De Porzelli P;  
 PI Haupt A, Janitschke L, Janssen B, Karl U, Kling A;  
 PI Mueller S, Ritter K, Thyos M, Zierke T;  
 XX  
 XX WPI; 1995-393582/51.  
 DR  
 XX  
 XX Prepn. of proline contg. tetra-peptide derivs. - comprises  
 FT condensing tri-peptide with protected amino acid, deprotection, and  
 PT N-di-methylation, useful as e.g. intermediates for dolastatin  
 XX  
 XX Example 4; Page 6; 8pp; German.  
 PS  
 XX  
 CC This invention describes a method for the production of tetrapeptides  
 CC which comprises reacting a tripeptide with an amino acid, removing Z and  
 CC methylating the free amino group twice. R1, R4 = 1-6C alkyl; and Z =  
 CC optional ring substituted benzyloxycarbonyl. The products of the  
 CC invention are intermediates for dolastatin 15 which have high  
 CC antineoplastic activity. The peptides of the invention are active against  
 CC solid tumours (of lung, breast, intestine, bladder, rectum, uterus and  
 CC prostate), leukaemia, lymphoma and other neoplastic diseases. The  
 CC peptides can now be produced from material available in large quantities,  
 CC without racemisation and without requiring very expensive or hazardous  
 CC reagents.  
 XX  
 XX  
 SQ Sequence 4 AA;  
 Query Match 65.0%; Score 13; DB 16; Length 4;  
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 VLEP 4  
 DB 1 VLVP 4  
 RESULT 22  
 AAW62052  
 ID AAW62052 standard; peptide; 4 AA.  
 XX  
 AC AAW62052;  
 XX

DT 11-SEP-1998 (first entry)  
 XX  
 DE Human erythropoietin peptide fragment T13.  
 XX  
 KW Human, erythropoietin; EPO, bone marrow, reticulocyte; red blood cell;  
 KW expression; CHO, Chinese hamster ovary cell; diagnosis; blood disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN AU688723-B.  
 XX  
 PD 19-FEB-1998.  
 XX  
 XX 02-DEC-1997; 97AU-0046867.  
 PF  
 XX 02-DEC-1997; 97AU-0046867.  
 PR  
 XX (KIP1 ) KIPIN AMGEN INC.  
 PA  
 PI Lin F;  
 XX  
 XX WPI; 1998-261957/24.  
 DR  
 XX Recombinant human erythropoietin - potentially useful for diagnosis  
 PT and treatment of blood disorders  
 FT  
 XX Example 1, Page 25; 100pp; English.  
 PS  
 XX The present sequence represents a peptide fragment of human  
 CC erythropoietin (EPO). The present invention describes recombinant  
 CC human EPO which causes bone marrow cells to increase production  
 CC of reticulocytes or red blood cells, where the polypeptide is the  
 CC product of expression in CHO (Chinese hamster ovary) cells of an  
 CC exogenous DNA sequence encoding human EPO. EPO is potentially  
 CC useful in the diagnosis and treatment of blood disorders  
 CC characterised by low or defective red blood cell production.  
 XX  
 XX  
 SQ Sequence 4 AA;  
 Query Match 65.0%; Score 13; DB 19; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 VLE 3  
 DB 1 VLE 3  
 RESULT 23  
 AAY15644  
 ID AAY15644 standard; Peptide; 4 AA.  
 XX  
 AC AAY15644;  
 XX  
 DT 27-JUL-1999 (first entry)  
 XX  
 XX Peptide used to make fluorescent reporter molecules.  
 DE  
 XX Fluorogenic; fluorescent reporter molecule; enzyme substrate;  
 KW apoptosis; protease; peptidase; apoptosis cascade; cancer;  
 KW chemotherapeutic agent; cell death; viral fitness activity.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9918856-A1.  
 PN  
 XX 22-APR-1999.  
 PD  
 XX 09-OCT-1998; 98WO US21231.  
 PF  
 XX 03-MAR-1998; 98US-0033661.  
 PR  
 XX 10-OCT-1997; 97US-0061582.  
 XX

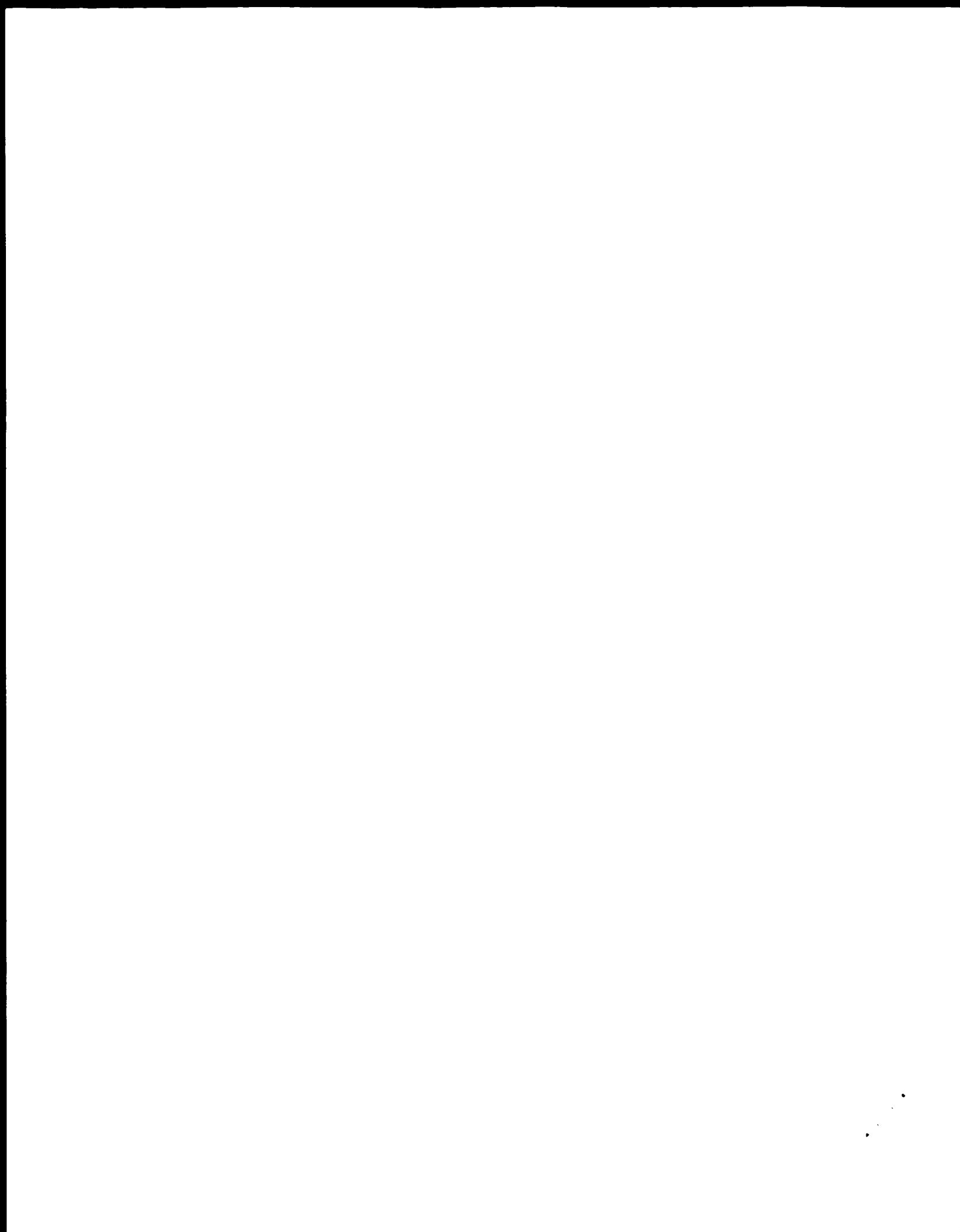
PA (CYTO-) CYTOVIA INC.  
XX Cai SX, Drewe JA, Keana JFW, Weber E, Zhang H;  
XX WPI; 1999-312448/26.  
XX New fluorogenic or fluorescent reporter molecules  
PS Claim 6, Page 167, 202pp; English.  
XX  
XX AAY15618-Y15759 represent peptides used to make the fluorogenic or  
XX fluorescent reporter molecules of the invention. These molecules  
XX contain a peptide moiety (e.g. present sequence) which acts as a  
XX substrate for enzymes involved in apoptosis or protease or peptidase  
XX enzymes. The compounds can be used as fluorogenic or fluorescent  
XX substrates for enzymes. Depending on the peptide moiety used, the  
XX fluorescent molecules can be used for detecting or measuring the  
XX activity of an enzyme involved in the apoptosis cascade in cells; to  
XX determine whether a test compound has an effect on an enzyme involved  
XX in the apoptosis cascade in cells; for determining the sensitivity of  
XX an animal with cancer to treatment with chemotherapeutic agents or  
XX enhancing cell death of test cells; for detecting or measuring the  
XX activity of a viral protease in cells; for determining whether a test  
XX compound has an effect on the activity of a viral protease in cells,  
XX and for measuring the activity or determining whether a test substance  
XX has an effect on the activity of a protease or peptidase in cells.  
SQ Sequence 4 AA;  
Query Match 65.0%; Score 13; DB 20; Length 4;  
Best Local Similarity 66.7%; Pred No. 7.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LEP 4  
DB 1 VEP 3  
RESULT 24  
AAW83445  
ID AAW83445 standard; peptide; 4 AA.  
XX  
XX AAW83445;  
XX  
XX  
XX 08-MAR-1999 (first entry)  
XX Human growth hormone mutant peptide #5.  
XX  
XX Human; growth hormone; hGH; phagemid particle; enzyme substrate;  
XX fusion gene; phage protein coat.  
XX  
XX Homo sapiens.  
XX Synthetic.  
XX  
XX US5946765-A.  
XX  
XX 08-DEC-1999.  
XX  
XX 16-MAY-1995; 95US-0441871.  
XX  
XX 02-DEC-1993; 93US-0161692.  
XX 03-DEC-1990; 90US-0621667.  
XX 10-APP-1991; 91US-0683400.  
XX 14-JUN-1991; 91US-0715300.  
XX 09-AUG-1991; 91US-0743614.  
XX 03-DEC-1991; 91MO-0509133.  
XX 06-APP-1992; 92US-0864452.  
XX 10-APP-1993; 93US-0050058.  
XX 05-APP-1995; 95US-0418928.  
XX 16-MAY-1995; 95US-0441871.  
XX (GETH ) GENENTECH INC.  
PA  
XX Matthews DJ, Wells JA, Zoller MJ;  
XX WPI; 1999-059058/05.  
XX  
XX Selection of polypeptide substrates - using phagemid particles  
XX displaying polypeptide(s) as coat protein fusions  
PS Example 8; Column 32; 81pp; English.  
XX  
XX The present invention describes a method for selecting novel polypeptide  
XX substrates. The method comprises: (a) constructing a replicable  
XX expression vector comprising a transcription regulatory element operably  
XX linked to a gene fusion; (b) mutating the vector at one or more selected  
XX positions within the second gene thereby forming a family of related  
XX plasmids encoding substrate peptides; (c) transforming suitable host  
XX cells with the plasmids; (d) infecting the transformed host cells with a  
XX helper phage having a gene encoding the phage coat protein; (e) culturing  
XX the transformed infected host cells under conditions suitable for forming  
XX recombinant phagemid particles containing at least a portion of the  
XX plasmid and capable of transforming the host; the conditions being  
XX adjusted so that no more than a minor amount of phagemid particles  
XX display more than one copy of the fusion protein on the surface of the  
XX particle; (f) exposing the phagemid particles to a process capable of  
XX modifying at least one covalent bond of an amino acid in the substrate  
XX peptide of at least a portion of the phagemid particles; (g) contacting  
XX the family of exposed phagemid particles with an affinity molecule, where  
XX the affinity molecule has affinity for the amino acid residue having the  
XX modified covalent bond; and (h) separating the phagemid particles that  
XX bind to the affinity molecule from those that do not bind. The selection  
XX method is used for identifying enzyme substrates. The present sequence  
XX represents a human growth hormone mutant peptide from an example of the  
XX present invention.  
SQ Sequence 4 AA;  
Query Match 65.0%; Score 13; DB 20; Length 4;  
Best Local Similarity 66.7%; Pred No. 7.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LEP 4  
DB 2 LDP 4  
RESULT 25  
AAY80808  
ID AAY80808 standard; peptide; 4 AA.  
XX  
XX AAY80808;  
XX  
XX 22 MAY-2000 (first entry)  
XX  
XX Fluorophore-labelled granzyme B substrate peptide, SEQ ID NO:27.  
XX  
XX Protease substrate; fluorescent label; fluorophore; rhodamine;  
XX blocking group; halogenoaryl group; cleavage; catpase; viral protease;  
XX methionine aminopeptidase type 2; MetAP 2; drug screening.  
XX  
XX Synthetic.  
XX  
XX WC200004914-A1  
XX  
XX 03-FEB-2000.  
XX  
XX 21-JUL-1999; 99WO-US16423.  
XX  
XX 21-JUL-1999; 99US-0093642.  
XX  
XX (CYTO-) CYTOVIA INC.  
XX (ZHAN/) ZHANG H.  
XX (CAIS/) CAI S X.  
XX (DREW/) DREWE J A.  
PA

PA (YANG/) YANG W.  
 XX Zhang H, Cai SX, Drewe JA, Yang W;  
 XX WPI: 2000-195079/17  
 XX New fluorescently labeled amino acids or peptides, used as substrates  
 PT for detecting enzymes or their modulators, e.g. anticancer or antiviral  
 PT agents, contains a halobenzoyl N-blocking group  
 XX  
 PS Claim 3; Page 100; 174pp; English.  
 XX  
 CC The invention relates to fluorescently labelled peptides containing  
 CC a halobenzoyl group on the fluorophore. They are of the structure  
 CC peptide-Y-Z, where Z represents a halo-substituted benzoyl blocking  
 CC group, Y is a fluorescent or fluorogenic moiety (preferably a  
 CC rhodamine), and the peptide-Y bond is cleavable by the enzyme being  
 CC assayed. The labelled peptides are reporters for detecting intracellular  
 CC proteolytic enzymes, particularly caspases and other enzymes involved in  
 CC apoptosis; viral proteases (e.g., HIV, herpes simplex virus-1, human  
 CC cytomegalovirus and hepatitis C virus proteases); and methionine  
 CC aminopeptidase type 2 (MetAP-2). The peptides are particularly used to  
 CC identify modulators of these enzymes which may be potentially useful as  
 CC agents for treating conditions such as cancer, neurodegeneration,  
 CC autoimmune diseases, myocardial infarction and viral infection.  
 CC Modulators identified may also be used to prolong the life of cells being  
 CC cultured for recombinant protein production, or to monitor the treatment  
 CC of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are  
 CC potential anti-angiogenic or anticancer agents. Sequences  
 CC AAYAN742 yanq16 represent peptides, some of which are specifically  
 CC claimed, which may be used in assay methods according to the invention.  
 XX  
 SQ Sequence 4 AA;

Query Match 65.0%; Score 13; DB 21; Length 4;  
 Best local Similarity 66.7%; Pred.No. 7.4e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0, Gaps 0;

OY 2 LEP 4  
 DB 1 VEP 3

Search completed: March 5, 2003, 08:38:32  
 Job time : 34 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run 3: Mar 5, 2003, 09:43:30, Search time: 14.34 mins  
(without alignment)  
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Title: US-09-732-411-15

Perfect score: 20

Sequence: 1 VLEP 4

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 18454 seqs, 42170167 residues

Total number of hits satisfying chosen parameters: 1965

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

# SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	20	100.0	4	10 US-09-729-873-16	Sequence 16, Appl
2	20	100.0	4	10 US-09-732-411-15	Sequence 15, Appl
3	14	70.0	4	10 US-09-729-873-24	Sequence 24, Appl
4	14	70.0	4	10 US-09-947-387-23	Sequence 23, Appl
5	13	65.0	4	10 US-09-947-387-27	Sequence 27, Appl
6	12	60.0	4	9 US-10-087-905-8	Sequence 8, Appl
7	12	60.0	4	10 US-09-947-387-13	Sequence 13, Appl
8	11	55.0	4	9 US-09-947-387-16	Sequence 16, Appl
9	10	50.0	4	10 US-09-031-629A-1	Sequence 1, Appl
10	10	50.0	4	8 US-08-494-409-26	Sequence 25, Appl
11	10	50.0	4	9 US-09-742-096-26	Sequence 26, Appl
12	10	50.0	4	9 US-10-029-191-16	Sequence 16, Appl
13	10	50.0	4	9 US-10-115-704-9	Sequence 9, Appl
14	10	50.0	4	9 US-10-207-951-8	Sequence 8, Appl
15	10	50.0	4	9 US-10-207-951-9	Sequence 9, Appl
16	10	50.0	4	10 US-09-729-873-21	Sequence 21, Appl
17	10	50.0	4	10 US-09-804-017-4	Sequence 4, Appl
18	10	50.0	4	10 US-09-934-765-742	Sequence 742, App
19	10	50.0	4	10 US-09-904-733A-3	Sequence 3, Appl

20	9	45.0	3	10 US-09-729-873-16	Sequence 16, Appl
21	9	45.0	4	8 US-08-484-409-13	Sequence 13, Appl
22	9	45.0	4	8 US-08-484-409-13	Sequence 13, Appl
23	9	45.0	4	9 US-09-947-387-23	Sequence 23, Appl
24	9	45.0	4	9 US-09-947-387-27	Sequence 27, Appl
25	9	45.0	4	9 US-10-087-905-8	Sequence 8, Appl
26	9	45.0	4	9 US-10-115-704-9	Sequence 9, Appl
27	9	45.0	4	9 US-10-207-951-8	Sequence 8, Appl
28	9	45.0	4	9 US-10-207-951-9	Sequence 9, Appl
29	9	45.0	4	10 US-09-729-873-21	Sequence 21, Appl
30	9	45.0	4	10 US-09-804-017-4	Sequence 4, Appl
31	9	45.0	4	10 US-09-934-765-742	Sequence 742, Appl
32	9	45.0	4	10 US-09-904-733A-3	Sequence 3, Appl
33	9	45.0	4	10 US-09-947-387-23	Sequence 23, Appl
34	9	45.0	4	10 US-09-947-387-27	Sequence 27, Appl
35	9	45.0	4	10 US-10-087-905-8	Sequence 8, Appl
36	9	45.0	4	10 US-10-115-704-9	Sequence 9, Appl
37	9	45.0	4	10 US-10-207-951-8	Sequence 8, Appl
38	9	45.0	4	10 US-10-207-951-9	Sequence 9, Appl
39	9	45.0	4	10 US-09-729-873-21	Sequence 21, Appl
40	9	45.0	4	10 US-09-804-017-4	Sequence 4, Appl
41	9	45.0	4	10 US-09-934-765-742	Sequence 742, Appl
42	9	45.0	4	10 US-09-904-733A-3	Sequence 3, Appl
43	9	45.0	4	10 US-09-947-387-23	Sequence 23, Appl
44	9	45.0	4	10 US-09-947-387-27	Sequence 27, Appl
45	9	45.0	4	10 US-10-087-905-8	Sequence 8, Appl
46	9	45.0	4	10 US-10-115-704-9	Sequence 9, Appl
47	9	45.0	4	10 US-10-207-951-8	Sequence 8, Appl
48	9	45.0	4	10 US-10-207-951-9	Sequence 9, Appl
49	9	45.0	4	10 US-09-729-873-21	Sequence 21, Appl
50	9	45.0	4	10 US-09-804-017-4	Sequence 4, Appl

## ALIGNMENTS

### RESULT 1

US-09-729-873-16  
Sequence 16, Application US/09729873  
Patent No. US001003621A1  
GENERAL INFORMATION:  
APPLICANT: Sany Ashkar  
TITLE OF INVENTION: Ostracod-in-Derived Characteristic and Inhibitory Agents  
FILE REFERENCE: CMZ-123CP  
CURRENT APPLICATION NUMBER: US/09/729,873  
CURRENT FILING DATE: 2000-12-05  
PRIOR APPLICATION NUMBER: 60/129,764  
PRIOR FILING DATE: 1999-04-15  
PRIOR APPLICATION NUMBER: PCT/US00/10344  
PRIOR FILING DATE: 2000-04-17  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 16  
LENGTH: 4  
TYPE: PPT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide  
US-09-729-873-16

Query Match 100.0% Score 20; DB 10; Length 4;  
Pos. Local Similarity 100.0%; Pred No 1 6405;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4

Db 1 VLEP 4

### RESULT 2

US-09-732-411-15

```

: Sequence 15, Application US/09732411
: Patent No. US20020058336A1
: GENERAL INFORMATION:
: APPLICANT: Samy Ashkar
: TITLE OF INVENTION: Adhesion Modulatory Peptides and Methods for Use
: FILE REFERENCE: CM2 124CP
: CURRENT APPLICATION NUMBER: US/09/732,411
: PRIORITY FILING DATE: 2000-12-07
: PRIOR APPLICATION NUMBER: 60/129,769
: PRIOR FILING DATE: 1999-04-16
: PRIOR APPLICATION NUMBER: FT/US09/10323
: PRIOR FILING DATE: 2000-04-17
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 15
: LENGTH: 4
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-732-411-15

Query Match 100.0%; Score 20; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
Db 1 VLEP 4

RESULT 3
US-09-732-873-24
: Sequence 24, Application US/09729873
: Patent No. US20020058336A1
: GENERAL INFORMATION:
: APPLICANT: Samy Ashkar
: TITLE OF INVENTION: Osteopontin Derived Chemotactic and Inhibitory Agents
: FILE REFERENCE: CM2-123CP
: CURRENT APPLICATION NUMBER: US/09/729,873
: PRIORITY FILING DATE: 2000-12-05
: PRIOR APPLICATION NUMBER: 60/123,764
: PRIOR FILING DATE: 1999-04-15
: PRIOR APPLICATION NUMBER: FT/US09/10344
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 24
: LENGTH: 4
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
: NAME/KEY: MLD PES
: LOCATION: 11
: OTHER INFORMATION: ACETYLATION
US-09-729-873-24

Query Match 70.0%; Score 14; DB 10; Length 4;
Best Local Similarity 60.0%; Pred. No 1.6e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
Db 1 MLDP 4

RESULT 4
US-09-947-387-23
: Sequence 23, Application US/09947387

```

```

: Patent No. US20020150885A1
: GENERAL INFORMATION:
: APPLICANT: Weber, Eckard
: APPLICANT: Cai, Sui Xiong
: APPLICANT: Keana, John P.W.
: APPLICANT: Drewe, John A.
: APPLICANT: Zhang, Han Zhong
: TITLE OF INVENTION: DC US20020150885A1 Fluorogenic or Fluorescent Reporter Molecule
: TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
: TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
: TITLE OF INVENTION: Use Thereof
: FILE REFERENCE: 1735 0290005
: CURRENT APPLICATION NUMBER: US/09/947,387
: CURRENT FILING DATE: 2001-09-07
: PRIOR APPLICATION NUMBER: US 60/061,582
: PRIOR FILING DATE: 1997-10-10
: PRIOR APPLICATION NUMBER: US 60/145,746
: PRIOR FILING DATE: 1998-03-03
: PRIOR APPLICATION NUMBER: US 09/168,888
: PRIOR FILING DATE: 1998-10-09
: NUMBER OF SEQ ID NOS: 142
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 23
: LENGTH: 4
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
: OTHER INFORMATION: Peptide
US-09-947-387-23

Query Match 70.0%; Score 14; DB 10; Length 4;
Best Local Similarity 66.7%; Pred. No 1.6e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4
Db 1 LEP 3

RESULT 5
US-09-947-387-27
: Sequence 27, Application US/09947387
: Patent No. US20020150885A1
: GENERAL INFORMATION:
: APPLICANT: Weber, Eckard
: APPLICANT: Cai, Sui Xiong
: APPLICANT: Keana, John P.W.
: APPLICANT: Drewe, John A.
: APPLICANT: Zhang, Han Zhong
: TITLE OF INVENTION: DC US20020150885A1 Fluorogenic or Fluorescent Reporter Molecule
: TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
: TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
: TITLE OF INVENTION: Use Thereof
: FILE REFERENCE: 1735 0290005
: CURRENT APPLICATION NUMBER: US/09/947,387
: CURRENT FILING DATE: 2001-09-07
: PRIOR APPLICATION NUMBER: US 60/061,582
: PRIOR FILING DATE: 1997-10-10
: PRIOR APPLICATION NUMBER: US 60/145,746
: PRIOR FILING DATE: 1998-03-03
: PRIOR APPLICATION NUMBER: US 09/168,888
: PRIOR FILING DATE: 1998-10-09
: NUMBER OF SEQ ID NOS: 142
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 27
: LENGTH: 4
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
: OTHER INFORMATION: Peptide
US-09-947-387-27

```

Query Match 65.0%; Score 13; DB 10; Length 4;  
 Best Local Similarity 66.7%; Pred No 1.6e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4  
 :||  
 Db 1 VEP 3

RESULT 6  
 US-10-087-905-8  
 ; Sequence 8, Application US/10087905  
 ; Publication No. US20030022152A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Haaland, Perry D.  
 ; APPLICANT: Sherman, Douglas B.  
 ; APPLICANT: Stewart II, Walter W.  
 ; APPLICANT: Lloyd, Sheila A.  
 ; APPLICANT: Campbell, Robert L.  
 ; TITLE OF INVENTION: METHODS, APPARATUS AND COMPUTER PROGRAMS FOR  
 ; FILE REFERENCE: P3250  
 ; CURRENT APPLICATION NUMBER: US/10/087,905  
 ; CURRENT FILING DATE: 2002-03-05  
 ; PRIOR APPLICATION NUMBER: US/09/359,260  
 ; PRIOR FILING DATE: 1999-07-22  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 8  
 ; LENGTH: 4  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: hypothetical  
 ; OTHER INFORMATION: peptide  
 ; US 10-087-905-8

Query Match 60.0%; Score 12; DB 9; Length 4;  
 Best Local Similarity 100.0%; Pred No. 1.6e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EP 4  
 :||  
 Db 3 EP 4

RESULT 7  
 US-09-947-387-13  
 ; Sequence 13, Application US/09947387  
 ; Patent No. US2002015084A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weber, Eckard  
 ; APPLICANT: Cai, Sui Xiong  
 ; APPLICANT: Keana, John F.W.  
 ; APPLICANT: Drewe, John A.  
 ; APPLICANT: Zhang, Han Zhong  
 ; TITLE OF INVENTION: NO. US2002015084A1 Fluorogenic or Fluorescent Reporter Molecu  
 ; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
 ; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
 ; TITLE OF INVENTION: Use Thereof  
 ; FILE REFERENCE: 1716.0290005  
 ; CURRENT APPLICATION NUMBER: US/09/947,387  
 ; CURRENT FILING DATE: 2001-09-07  
 ; PRIOR APPLICATION NUMBER: US 60/061,582  
 ; PRIOR FILING DATE: 1997-10-10  
 ; PRIOR APPLICATION NUMBER: US 60/145,746  
 ; PRIOR FILING DATE: 1998-03-03  
 ; PRIOR APPLICATION NUMBER: US 09/168,888  
 ; PRIOR FILING DATE: 1998-10-09  
 ; NUMBER OF SEQ ID NOS: 142  
 ; SOFTWARE: Patent In Ver 2.0  
 ; SEQ ID NO 13

LENGTH: 4  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 OTHER INFORMATION: Peptide  
 US-09-947-387-13

Query Match 60.0%; Score 12; DB 10; Length 4;  
 Best Local Similarity 100.0%; Pred No 1.6e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EP 4  
 :||  
 Db 2 EP 3

RESULT 8  
 US-09-861-097-16  
 ; Sequence 16, Application US/09861097  
 ; Publication No. US20020102218A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KARIN, MICHAEL  
 ; APPLICANT: DAVIS, ROGER  
 ; APPLICANT: MASAHITO, HIBI  
 ; APPLICANT: ANNING, LIN  
 ; APPLICANT: BERLIARD, BENOIT  
 ; TITLE OF INVENTION: ONCOGENIC PROTEIN KINASE  
 ; NUMBER OF SEQUENCES: 25  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FISH & RICHARDSON P.C.  
 ; STREET: 4225 Executive Square, Suite 1400  
 ; CITY: La Jolla  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 92037  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/861,097  
 ; FILING DATE: 18-May-2001  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/220,602  
 ; FILING DATE: 25-MAR-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Haile, Ph.D., Lisa A.,  
 ; REGISTRATION NUMBER: 38,347  
 ; REFERENCE/SEQ ID NO: 16;  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (619) 678-5070  
 ; TELEFAX: (619) 678-5099  
 ; INFORMATION FOR SEQ ID NO: 16:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; FEATURE:  
 ; NAME/KEY: Peptide  
 ; LOCATION: 1..4  
 ; OTHER INFORMATION /note "seq - Leu or Ala, Asp - Asp  
 ; or Glu"  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
 ; US-09-861-097-16

Query Match 55.0%; Score 11; DB 9; Length 4;  
 Best Local Similarity 66.7%; Pred No 1.6e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 2 LEP 4
DB 1 LEP 3

RESULT 9
US-09-031-629A-3
; Sequence 3, Application US/09031629A
; Patent No. US20020155441A1
; GENERAL INFORMATION:
; APPLICANT: Hayashi
; TITLE OF INVENTION: Methods for Treating and Diagnosing Autoimmune Disease
; FILE REFERENCE: MWR/Raustman 17633/1050
; CURRENT APPLICATION NUMBER: US/09/031,629A
; PRIORITY FILING DATE: 1998-02-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fluorogenic
; OTHER INFORMATION: Peptide used for degradation assays
; NAME/KEY: SITE
; LOCATION: 131
; OTHER INFORMATION: Beta Lactamylamide is attached to the C-terminal
; OTHER INFORMATION: Glu
; NAME/KEY: SITE
; LOCATION: 131
; OTHER INFORMATION: The N-terminal Leu contains a carbonyl group
; OTHER INFORMATION: modification
US-09-031-629A-3

Query Match 50.0%; Score 10; DB 10; Length 3;
Best Local Similarity 66.7%; Pred No 1;6e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
DB 1 LLE 3

RESULT 10
US-08-484-409-25
; Sequence 25, Application US/08484409
; Patent No. US20030076412A1
; GENERAL INFORMATION:
; APPLICANT: Steinman, Lawrence
; TITLE OF INVENTION: METHODS FOR MODULATING THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 201 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104 7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.0
; CURRENT AFFILIATION DATA:
; APPLICATION NUMBER: US/08/484,409
; FILING DATE: 07 JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392

QY 1 VLE 3
DB 1 LLE 3

RESULT 11
US-09-742-096-26
; Sequence 26, Application US/09742096
; Patent No. US20020155441A1
; GENERAL INFORMATION:
; APPLICANT: DPHULHE, PIERRE
; TITLE OF INVENTION: MALAPIAL PRE-EPYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
; FILE REFERENCE: 200773050DIV
; CURRENT APPLICATION NUMBER: US/09/742,096
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 08/973,642
; PRIOR FILING DATE: 1998-02-06
; PRIOR APPLICATION NUMBER: PCT/EP96/00894
; PRIOR FILING DATE: 1996-06-12
; PRIOR APPLICATION NUMBER: EP 95/07007
; PRIOR FILING DATE: 1995-06-13
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 26
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-742-096-26

Query Match 50.0%; Score 10; DB 9; Length 4;
Best Local Similarity 66.7%; Pred No 1;6e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
DB 1 VVE 3

RESULT 12
US-10-029-191-16
; Sequence 16, Application US/10029191
; Patent No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A.J.
; TITLE OF INVENTION: NEWFL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 210147, 00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/560,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 06/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
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; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Rattus sp.  
; US-10-029-191-16

Query Match 50.0%; Score 10; DB 9; Length 4;  
Best Local Similarity 66.7%; Pred No. 1.6e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3  
|||  
DB 2 VVE 4

RESULT 13  
US-10-115-704-9  
; Sequence 9, Application US/10115704  
; Publication No. US20030013156A1  
; GENERAL INFORMATION:  
; APPLICANT: SOHN, JOON HONG  
; APPLICANT: KIM, JOO YOUNG  
; TITLE OF INVENTION: NOVEL ANTI INFLAMMATORY PEPTIDES  
; FILE REFERENCE: CL000663CON  
; CURRENT APPLICATION NUMBER US/10/207,951  
; PRIOR FILING DATE: 2002-07-31  
; PRIOR APPLICATION NUMBER: KR10 2001 21599  
; PRIOR FILING DATE: 2001-04-21  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Kopatent In 1.71  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC  
US-10-115-704-9

Query Match 50.0%; Score 10; DB 9; Length 4;  
Best Local Similarity 66.7%; Pred No. 1.6e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3  
|||  
DB 2 VLD 4

RESULT 14  
US-10-207-951-8  
; Sequence 9, Application US/10207951  
; Publication No. US20030013156A1  
; GENERAL INFORMATION:  
; APPLICANT: Karl GUEGLER et al.  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; FILE REFERENCE: NUCLEIC ACID SEQUENCES ENCODING HUMAN TRANSPORTER PROTEINS  
; FILE REFERENCE: AND USES THEREOF  
; CURRENT APPLICATION NUMBER: US/10/207,951  
; PRIOR FILING DATE: 2002-07-31  
; PRIOR APPLICATION NUMBER: 09/735,932  
; PRIOR FILING DATE: 2000-12-14  
; PRIOR APPLICATION NUMBER: 60/211,223  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-207-951-8

Query Match 50.0%; Score 10; DB 9; Length 4;

Best Local Similarity 66.7%; Pred No. 1.6e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3  
|||  
DB 2 LLE 4

RESULT 15  
US-10-207-951-3  
; Sequence 9, Application US/10207951  
; Publication No. US20030013156A1  
; GENERAL INFORMATION:  
; APPLICANT: Karl GUEGLER et al.  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; FILE REFERENCE: NUCLEIC ACID SEQUENCES ENCODING HUMAN TRANSPORTER PROTEINS  
; FILE REFERENCE: AND USES THEREOF  
; CURRENT APPLICATION NUMBER: US/10/207,951  
; PRIOR FILING DATE: 2002-07-31  
; PRIOR APPLICATION NUMBER: 09/735,932  
; PRIOR FILING DATE: 2000-12-14  
; PRIOR APPLICATION NUMBER: 60/211,223  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-207-951-9

Query Match 50.0%; Score 10; DB 9; Length 4;  
Best Local Similarity 66.7%; Pred No. 1.6e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3  
|||  
DB 2 LLE 4

RESULT 16  
US-09-729-873-21  
; Sequence 21, Application US/09729873  
; Patent No. US20010036921A1  
; GENERAL INFORMATION:  
; APPLICANT: Samy Ashkar  
; TITLE OF INVENTION: Osteopontin-Derived Chemotactic and Inhibitory Agents  
; FILE REFERENCE: CMZ 123CP  
; CURRENT APPLICATION NUMBER: US/09/729,873  
; CURRENT FILING DATE: 2000-12-05  
; PRIOR APPLICATION NUMBER: 60/129,764  
; PRIOR FILING DATE: 1999-04-15  
; PRIOR APPLICATION NUMBER: PCT/US00/10344  
; PRIOR FILING DATE: 2000-04-17  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence-Synthetic  
US-09-729-873-21

Query Match 50.0%; Score 10; DB 10; Length 4;  
Best Local Similarity 33.3%; Pred No. 1.6e+05;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4  
|||

Db 1 VDP 3

## RESULT 17

US-09-808-037-4

; Sequence 4, Application US/09808037

; Patent No. US2002005231A1

; GENERAL INFORMATION:

; APPLICANT: SOLOMON, Beka

; APPLICANT: HANAN, Eliad

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF

; TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS

; FILE REFERENCE: SOLOMON-25

; CURRENT APPLICATION NUMBER: US/09/808,037

; CURRENT FILING DATE: 2001-03-15

; PRIOR APPLICATION NUMBER: 09/629,971

; PRIOR FILING DATE: 2000-07-31

; PRIOR APPLICATION NUMBER: US 09/473,653

; PRIOR FILING DATE: 1999-12-29

; PRIOR APPLICATION NUMBER: US 60/152,417

; PRIOR FILING DATE: 1999-09-03

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 4

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: synthetic peptide

US-09-808-037-4

## Query Match

Best Local Similarity 50.0%; Score 10; DB 10; Length 4;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3

|||

Db 2 VLD 4

## RESULT 18

US-09-834-765-742

; Sequence 12, Application US/09834765

; Patent No. US2002005479A1

; GENERAL INFORMATION:

; APPLICANT: Mary Paris

; APPLICANT: Pia M. Challita-Bid

; APPLICANT: Arthur B. Raitano

; APPLICANT: Steve Chappell Mitchell

; APPLICANT: Daniel E.H. Afari

; APPLICANT: Aya Jakobovits

; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT

; TITLE OF INVENTION: AND DETECTION OF CANCER

; FILE REFERENCE: 129,605U1

; CURRENT APPLICATION NUMBER: US/09/834,765

; CURRENT FILING DATE: 2001-09-21

; PRIOR APPLICATION NUMBER: 60/197,647

; PRIOR FILING DATE: 2000-04-11

; NUMBER OF SEQ ID NOS: 770

; SOFTWARE: Pse+Seq for Windows Version 4.0

; SEQ ID NO 742

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-834-765-742

## Query Match

Best Local Similarity 50.0%; Score 10; DB 10; Length 4;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3

|||

Db 2 VLD 4

## RESULT 19

US-09-804-733A-3

; Sequence 3, Application US/09804733A

; Patent No. US20020059656A1

; GENERAL INFORMATION:

; APPLICANT: Monsanto Company

; TITLE OF INVENTION: PEPTIDE-INDUCED PROTEINS CONTAINING REPEATING UNITS

; FILE REFERENCE: MTC6614.2

; CURRENT APPLICATION NUMBER: US/09/804,733A

; CURRENT FILING DATE: 2001-03-13

; PRIOR APPLICATION NUMBER: US 60/188,990

; PRIOR FILING DATE: 2000-03-13

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 3

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Eubrynnus pelamis

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: (1)...(4)

US-09-804-733A-3

## Query Match

Best Local Similarity 50.0%; Score 10; DB 10; Length 4;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4

|||

Db 1 WVVP 4

## RESULT 20

US-09-312-762A-12

; Sequence 12, Application US/09312762A

; Patent No. US20020115069A1

; GENERAL INFORMATION:

; APPLICANT: MIA HOROWITZ ET AL

; TITLE OF INVENTION: ENZYME CONTAINING SEVERAL PROTEINS

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina

; STREET: 2001 Jefferson Davis Highway, Suite 207

; CITY: Arlington

; STATE: Virginia

; COUNTRY: United States of America

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

; COMPUTER: TWINK-31\* Silhouette R407X

; OPERATING SYSTEM: MS DOS version 6.2

; OPERATING SYSTEM: Windows version 3.11

; SOFTWARE: Word for Windows version 2.0 converted to

; CURRENT APPLICATION DATA

; APPLICATION NUMBER: US/09/312,762A

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/026,898

; FILING DATE: 20 FEB 1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Friedman, Mark M.

; REGISTRATION NUMBER: 33,883

; REFERENCE/DOC# NUMBER: 016/10

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 972-3-562553

; TELEFAX: 972-3-562554

; TELEX:

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

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? LENGTH: 3
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
US-09-312 762A 12

Query Match 45.0%; Score 9; DB 10; Length 3;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EP 4
DB 1 DP 2

RESULT 21
US-08-484-409-13
? Sequence 13, Application US/08484409
? Patent No. US20020697412A1
? GENERAL INFORMATION:
? APPLICANT: Steinman, Lawrence
? APPLICANT: Zamvil, Scott
? TITLE OF INVENTION: METHODS FOR MODULATING THE IMMUNE SYSTEM
? NUMBER OF SEQUENCES: 52
? CORRESPONDENT ADDRESS:
? ADDRESSER: SEED and BERRY LLP
? STREET: 6300 Columbia Center, 701 Fifth Avenue
? CITY: Seattle
? STATE: Washington
? COUNTRY: USA
? ZIP: 98104-7092
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-WINDOWS
? SOFTWARE: Patent Release #1 0. Version #1 30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/484,409
? FILING DATE: 07-JUN-1995
? CLASSIFICATION: 424
? ATTORNEY/AGENT INFORMATION:
? NAME: Maki, David J.
? REGISTRATION NUMBER: 31,392
? REFERENCE/PROXY NUMBER: 60004 40001
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (206) 622-4900
? TELEFAX: (206) 682-6031
? INFORMATION FOR SEQ ID NO: 13:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 4 amino acids
? TYPE: amino acid
? STRANDEDNESS:
? TOPOLOGY: linear
US-08-484-409-13

Query Match 45.0%; Score 9; DB 8; Length 4;
Best Local Similarity 33.3%; Pred. No. 1.6e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
DB 2 ILD 4

RESULT 22
US-09-964-114-5
? Sequence 5, Application US/09964114
? Patent No. US20020156094A1
? GENERAL INFORMATION:
? APPLICANT: Albrecht, Hans P. et al.
? TITLE OF INVENTION: Sulfonamide Interleukin-1Beta Converting Enzyme
? INHIBITORS
? FILE REFERENCE: 22253-68736
```

```
? CURRENT APPLICATION NUMBER: US/09/964,114
? CURRENT FILING DATE: 2001-09-25
? PRIOR APPLICATION NUMBER: 09/284,423
? PRIOR FILING DATE: 1999-04-02
? PRIOR APPLICATION NUMBER: PCT/US97/18196
? PRIOR FILING DATE: 1999-10-09
? PRIOR APPLICATION NUMBER: 60/028,313
? PRIOR FILING DATE: 1996-10-11
? NUMBER OF SEQ ID NOS: 6
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 5
? LENGTH: 4
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? NAME/KEY: UNSURE
? LOCATION: (1)..(4)
? OTHER INFORMATION: Acetyl group attached to 5' end and PMA group
? OTHER INFORMATION: attached to 3' end
? OTHER INFORMATION: Description of Artificial Sequence Chemically
? OTHER INFORMATION: synthesized
US-09-964-114-5

Query Match 45.0%; Score 9; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LE 3
DB 1 LE 2

RESULT 23
US-09-900-936-7
? Sequence 7, Application US/09900936
? Patent No. US20020165141A1
? GENERAL INFORMATION:
? APPLICANT: Rodgers, Kathleen
? APPLICANT: diZerega, Gere
? TITLE OF INVENTION: Methods for Promoting Lentiviral Cell Proliferation
? TITLE OF INVENTION: or Differentiation
? FILE REFERENCE: 00-506-A
? CURRENT APPLICATION NUMBER: US/99/900,936
? CURRENT FILING DATE: 2001-07-09
? NUMBER OF SEQ ID NOS: 50
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 7
? LENGTH: 4
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: A1 (5-8)
US-09-900-936-7

Query Match 45.0%; Score 9; DB 9; Length 4;
Best Local Similarity 33.3%; Pred. No. 1.6e+05;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LEP 4
DB 1 IHP 3

RESULT 24
US-10-085-801A-1
? Sequence 1, Application US/10085801A
? Patent No. US20020169123A1
? GENERAL INFORMATION:
? APPLICANT: El-Deiry, Wafik S.
? APPLICANT: Kim, Kunhong
? TITLE OF INVENTION: Regulating Apoptosis in TRAIL-Resistant Cancer Cells
? WHILE PROMOTING NO US20020169123A1
? FILE REFERENCE: 22253-68736
```

```

; CURRENT APPLICATION NUMBER: US/10/085,801A
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: 60/271,674
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: commercially
; OTHER INFORMATION: available
US-10-085-801A-1

Query Match      45.0%; Score 9; DB 9; Length 4;
Best Local Similarity 100.0%; Pred No 1 6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LE 3
        ||
Db      1 LE 2

RESULT 25
US-10-101-487-101
; Sequence 101, Application US/10101487
; Patent No.: US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFOUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K
; APPLICANT: WAGGNER JR., DAVID W
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-10-101-487-101

Query Match      45.0%; Score 9; DB 9; Length 4;
Best Local Similarity 50.0%; Pred No 1 1.6e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 EP 4
        :|
Db      2 QP 3

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Search completed: March 5, 2003, 09:49:32  
Job time : 35 secs

GenCore version 5.1.3  
Copyright (c) 1991 - 2003 CompuGen Ltd

OM protein - protein search, using sw mode1

Run on: March 5, 2003, 09:37:56, Search time 29 Seconds  
(without alignments)  
4.05a Millibits all updates/sec

Title: US-09-732 411 15

Perfect score: 26

Sequence: 1 VLEP 4

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Seatched: 262174 seqs, 2942322 residues

Total number of hits satisfying chosen parameters: 9158

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database: Issued Patents AA\*

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2: /cgn2\_6/prodata/1/iaa/5B.COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/6A.COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/6B.COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/6C.COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

# SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	15	75.0	4	1	US-08-240-712-5
2	15	75.0	4	1	US-08-443-890-5
3	15	75.0	4	4	US-08-08A-562-5
4	15	75.0	4	5	PCT-US92 00752-5
5	14	70.0	4	1	US-08-336-343A-38
6	14	70.0	4	2	US-08-609-271-1
7	14	70.0	4	4	US-08-188-374-1
8	14	70.0	4	4	US-09-130-193-16
9	14	70.0	4	4	US-09-357-952-23
10	14	70.0	4	4	US-08-521-550-23
11	14	70.0	4	4	US-08-168-888-23
12	14	70.0	4	4	US-09-513-783A-100
13	13	65.0	4	2	US-08-441-871-29
14	13	65.0	4	4	US-09-330-970-16
15	13	65.0	4	4	US-09-330-970-14
16	13	65.0	4	4	US-08-859-345-31
17	13	65.0	4	4	US-09-357-952-27
18	13	65.0	4	4	US-08-521-550-27
19	13	65.0	4	4	US-08-168-888-27
20	13	65.0	4	4	US-09-187-859-199
21	12	60.0	4	1	US-07-714-167E-8
22	12	60.0	4	1	US-07-714-167E-11
23	12	60.0	4	1	US-07-729-153-7
24	12	60.0	4	1	US-08-122-546-1
25	12	60.0	4	1	US-08-280-443-39
26	12	60.0	4	1	US-08-457-459-39
27	12	60.0	4	1	US-08-224-968-5

28	12	60.0	4	1	US-08-555-678-39
29	12	60.0	4	1	US-08-477-508B-7
30	12	60.0	4	1	US-08-477-508B-31
31	12	60.0	4	2	US-08-609-271-2
32	12	60.0	4	2	US-08-609-271-3
33	12	60.0	4	2	US-08-609-271-4
34	12	60.0	4	2	US-08-609-271-5
35	12	60.0	4	2	US-08-764-319-1
36	12	60.0	4	3	US-08-482-088B-7
37	12	60.0	4	3	US-08-415-655-3
38	12	60.0	4	3	US-08-624-405-7
39	12	60.0	4	3	US-08-131-053A-1
40	12	60.0	4	3	US-08-131-053A-1
41	12	60.0	4	3	US-08-131-053A-1
42	12	60.0	4	4	US-08-188-374-2
43	12	60.0	4	4	US-08-188-374-3
44	12	60.0	4	4	US-08-188-374-4
45	12	60.0	4	4	US-08-188-374-5
46	12	60.0	4	4	US-08-931-271-10
47	12	60.0	4	4	US-08-931-271-10
48	12	60.0	4	4	US-08-931-271-10
49	12	60.0	4	4	US-08-931-271-10
50	12	60.0	4	4	US-08-931-271-10

## ALIGNMENTS

RESULT 1  
US-08-240-712-5  
; Sequence 5, Application US/09240712  
; Patent No. 5599907  
; GENPAT INFORMATION:  
; APPLICANT: ANDERSON, DAVID C.  
; APPLICANT: WATHEWS, ANTHONY JAMES  
; APPLICANT: STETLER, GARY L.  
; TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/240,712  
; FILING DATE: 09-MAY-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/09752  
; FILING DATE: 13-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COOPER, IVER P  
; REGISTRATION NUMBER: 28,005  
; REFERENCE/DOCKET NUMBER: ANDERSON-6  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202 628-5197  
; TELEFAX: 202-737-3508  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-240-712-5

Query Match 75.0%, Score 15, DB 1, Length 4;  
Best Local Similarity 75.0%; Pred No. 1 9e+05;  
Matches 3; Conservative 0; Mismatches 1, Indels 0, Gaps 0.

QY 1 VLSP 4  
|||  
Db 1 VLSP 4

## RESULT 2

US-08-443-890-5  
; Sequence 5, Application US/68443890  
; Patent No. 5739011  
; GENERAL INFORMATION:  
; APPLICANT: ANDERSON, DAVID C.  
; APPLICANT: MATTHEWS, ANTONY JAMES  
; APPLICANT: STETLER, GARY L.  
; TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC  
; TITLE OF INVENTION: HEMOGLOBINS  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Pat-soft Release #1.0, Version #1.05  
CURRENT APPLICATION DATA:  
APPLICATOR NUMBER: US/68/443,890  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 530  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/240,712  
FILING DATE: 09-MAY-1994  
APPLICATION NUMBER: PCT/US92/09752  
FILING DATE: 13-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: COOPER, IVER P  
REGISTRATION NUMBER: 28,005  
REFERENCE/PACKET NUMBER: ANDERSON-6-PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-629-5107  
TELEFAX: 202-737-3528  
TELEX: 249633  
INFORMATION FOR SEQ ID NO. 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-443-890-5

Query Match 75.0%, Score 15, DB 1, Length 4;  
Best Local Similarity 75.0%; Pred. No. 1.9e+05;  
Matches 3, Conservative 0, Mismatches 1, Indels 0, Gaps 0.

QY 1 VLSP 4  
|||  
Db 1 VLSP 4

## RESULT 3

US-09-058-562-5  
; Sequence 5, Application US/09058562A  
; Patent No. 6194256

## GENERAL INFORMATION:

APPLICANT: Anderson, David C.  
APPLICANT: Mathews, Antony James  
APPLICANT: Stetler, Gary L.  
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC HEMOGLOBINS  
FILE REFERENCE: PXR 2087  
CURRENT APPLICATION NUMBER: US/09/058,562A  
CURRENT FILING DATE: 1998-04-13  
PRIOR APPLICATION NUMBER: US 08/240,712  
PRIOR FILING DATE: 1994-05-09  
PRIOR APPLICATION NUMBER: PCT/US92/09752  
PRIOR FILING DATE: 1993-05-13  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO: 5  
LENGTH: 4  
TYPE: PPT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: peptide  
US-09-058-562-5

Query Match 75.0%, Score 15, DB 4, Length 4;  
Best Local Similarity 75.0%; Pred No. 1 9e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLSP 4  
|||  
Db 1 VLSP 4

## RESULT 4

PCT-US92-09752-5  
; Sequence 5, Application PCT/US9209752  
; GENERAL INFORMATION:  
; APPLICANT: ANDERSON, DAVID C.  
; APPLICANT: MATTHEWS, ANTONY JAMES  
; APPLICANT: STETLER, GARY L.  
; TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC  
; TITLE OF INVENTION: HEMOGLOBINS  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Pat-soft Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/09752  
FILING DATE: 1993-01-09  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: COOPER, IVER P  
REGISTRATION NUMBER: 28,005  
REFERENCE/PACKET NUMBER: ANDERSON-6-PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-629-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO. 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US92-09752-5

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Query Match          75.0%; Score 15; DB 5; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLEP 4
   |||
Db 1 VLSP 4

RESULT 5
US-08-336-343A-38
; Sequence 38, Application US/08336343A
; Patent No. 5677144
; GENERAL INFORMATION:
; APPLICANT: Ulrich, Axel
; APPLICANT: Alvers, Frank
; TITLE OF INVENTION: c-Myb, A Myc-Related Protein Tyrosine Kinase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,343A
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7681-065
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 860-9741/9864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-336-343A-38

Query Match          70.0%; Score 14; DB 1; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LRP 4
   |||
Db 2 MRP 4

RESULT 6
US-08-600-271-1
; Sequence 1, Application US/08600271
; Patent No. 5811264
; GENERAL INFORMATION:
; APPLICANT: Aitken, Jacqueline F.
; APPLICANT: Apostol, Izydor Z.
; APPLICANT: Lippincott, Julie A.
; TITLE OF INVENTION: Proteins with Mutations to Decrease N-Terminal Methylation
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somatogen, Inc.

```

```

; STREET: 2545 Central Avenue, Site FD-1
; CITY: Boulder
; STATE: Colorado
; ZIP: 80301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.0.1
; SOFTWARE: Microsoft Word 5.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,271
; FILING DATE: 28 February 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/188,374
; FILING DATE: 1/27/94
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5811264elli, Marianne F.
; REGISTRATION NUMBER: 38571
; NAME: Brown, Theresa A.
; REGISTRATION NUMBER: 32547
; REFERENCE/DOCKET NUMBER: 170/Div
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-541-3324
; TELEFAX: 303-444-3013
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: no
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION /label=modified-site
; OTHER INFORMATION /label="Modified-site"
US-08-609-271-1

Query Match          70.0%; Score 14; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.9e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
   |||
Db 1 MLOP 4

RESULT 7
US-08-188-374-1
; Sequence 1, Application US/08188374B
; Patent No. 6140071
; GENERAL INFORMATION:
; APPLICANT: Aitken F., Jacqueline
; APPLICANT: Apostol, Izydor Z.
; APPLICANT: Lippincott, Julie A.
; APPLICANT: Levine, Joseph D.
; TITLE OF INVENTION: Proteins with Mutations to Decrease N-Terminal Methylation
; FILE REFERENCE: BXTB 1953
; CURRENT APPLICATION NUMBER: US/08/188,374B
; CURRENT FILING DATE: 1994 01 27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)
; OTHER INFORMATION: METHYLATION- N terminal Met
US-08-188-374-1

```

Query Match 70.0%, Score 14, DB 4, Length 4;  
 Best Local Similarity 50.0%, Pred. No. 1.9e+05;  
 Matches 2, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VLEP 4  
 :|||  
 DB 1 MLQP 4

## RESULT 8

US-09-130-193-16  
 ; Sequence 16, Application US/09130193  
 ; Patent No. 6235493  
 ; GENERAL INFORMATION:  
 ; APPLICANT: EUGENE R. BISSELL ET AL  
 ; TITLE OF INVENTION: AMINO ACID SUBSTITUTED-  
 ; CRESYL VIOLET, SYNTHETIC  
 ; TITLE OF INVENTION: FLUOREGENIC SUBSTRATES  
 ; TITLE OF INVENTION: FOR THE ANALYSIS OF  
 ; AGENTS IN INDIVIDUAL IN  
 ; VIVO CELLS OR TISSUE  
 ; NUMBER OF SEQUENCES: 16  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: PETERS, VERNY, JONES & BIK A, LLP  
 ; STREET: 385 Sherman Avenue, Suite 6  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: United States of America  
 ; ZIP: 94306-1840  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage  
 ; COMPUTER: PC  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: WordPerfect 5.1  
 ; CURRENT APPLICATION DATA  
 ; APPLICATION NUMBER: US/09/130,193  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/026,062  
 ; FILING DATE: SEPTEMBER 23, 1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: HOWARD T. PETERS  
 ; REGISTRATION NUMBER: 29,202  
 ; REFERENCE TO PARENT NUMBER: 3594 11-1 (HME)  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (650) 324-1677 X 10  
 ; TELEFAX: (650) 324-1678  
 ; INFORMATION FOR SEQ ID NO: 16:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: Peptide  
 ; US-09-130-193-16

Query Match 70.0%, Score 14, DB 4, Length 4;  
 Best Local Similarity 66.7%, Pred. No. 1.9e+05;  
 Matches 2, Conservative 1, Mismatches 0, Indels 0, Gaps 0;

QY 2 LEP 4  
 :|||  
 DB 1 IEP 3

## RESULT 9

US-09-357-952-23  
 ; Sequence 23, Application US/09357952  
 ; Patent No. 6248904  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zhang, Han-Zhong

; APPLICANT: Cai, Sui Xiong  
 ; APPLICANT: Drewe, John A  
 ; TITLE OF INVENTION: No 6248904el Fluorescence Dyes and Their Applications for Whole-Cell  
 ; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Proteases  
 ; TITLE OF INVENTION: Other Enzymes and the Use Thereof  
 ; FILE REFERENCE: 1735 0030001  
 ; CURRENT APPLICATION NUMBER: US/09/357,952  
 ; CURRENT FILING DATE: 1998-07-21  
 ; EARLIER APPLICATION NUMBER: US 60/093,642  
 ; EARLIER FILING DATE: 21-JUL-1998  
 ; NUMBER OF SEQ ID NOS: 139  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 23  
 ; LENGTH: 4  
 ; TYPE: PPT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Peptide  
 ; US 09 357-952-23

Query Match 70.0%, Score 14, DB 4, Length 4;  
 Best Local Similarity 66.7%, Pred. No. 1.9e+05;  
 Matches 2, Conservative 1, Mismatches 0, Indels 0, Gaps 0;

QY 2 LEP 4  
 :|||  
 DB 1 IEP 3

## RESULT 10

US-09-521-650-23  
 ; Sequence 23, Application US/09521650  
 ; Patent No. 6335429  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weber, Eckard  
 ; APPLICANT: Cai, Sui Xiong  
 ; APPLICANT: Keana, John F.W.  
 ; APPLICANT: Drewe, John A.  
 ; APPLICANT: Zhang, Han-Zhong  
 ; TITLE OF INVENTION: No 6335429el Fluorescent Reporter Molecules and  
 ; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
 ; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
 ; TITLE OF INVENTION: Use Thereof  
 ; FILE REFERENCE: 1735 0040002  
 ; CURRENT APPLICATION NUMBER: US/09/521,650  
 ; CURRENT FILING DATE: 2000-03-08  
 ; EARLIER APPLICATION NUMBER: 09/169,888  
 ; EARLIER FILING DATE: 1998-10-09  
 ; EARLIER APPLICATION NUMBER: US 60/061,592  
 ; EARLIER FILING DATE: 1997-10-10  
 ; EARLIER APPLICATION NUMBER: US 09/033,661  
 ; EARLIER FILING DATE: 1998-03-03  
 ; NUMBER OF SEQ ID NOS: 142  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 23  
 ; LENGTH: 4  
 ; TYPE: PPT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Peptide  
 ; US-09-521-650-23

Query Match 70.0%, Score 14, DB 4, Length 4;  
 Best Local Similarity 66.7%, Pred. No. 1.9e+05;  
 Matches 2, Conservative 1, Mismatches 0, Indels 0, Gaps 0;

QY 2 LEP 4  
 :|||  
 DB 1 IEP 3



## RESULT 11

US-09-168-888-23  
Sequence 23, Application US/09168888  
Patent No. 6342611

## GENERAL INFORMATION:

APPLICANT: Weber, Eckard  
APPLICANT: Cai, Sui Xiong  
APPLICANT: Keane, John F W  
APPLICANT: Drewe, John A.  
APPLICANT: Zhang, Han-Zhong

TITLE OF INVENTION: No. 6342611 Fluorogenic or Fluorescent Reporter Molecules and  
TITLE OF INVENTION: Their Applications for Whole Cell Fluorescence  
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
TITLE OF INVENTION: Use Thereof

FILE REFERENCE: 1735.0290002  
CURRENT APPLICATION NUMBER: US/09/168,888

CURRENT FILING DATE: 1998-10-09  
EARLIER APPLICATION NUMBER: US 60/061,582

EARLIER FILING DATE: 1997-10-10

EARLIER APPLICATION NUMBER: US 09/033,661

EARLIER FILING DATE: 1998-03-03

NUMBER OF SEQ ID NOS: 142

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 23

LENGTH: 4

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide

US-09-168-888-23

Query Match  
Best Local Similarity 66.7%, Score 14, DB 4, Length 4,  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 LEP 4

DB 1 LEP 3

## RESULT 12

US-09-513-783A-100

Sequence 100, Application US/09513783A

Patent No. 6416959

## GENERAL INFORMATION:

APPLICANT: Giuliano, Kenneth A.

APPLICANT: Kapur, Ravi

TITLE OF INVENTION: A System for Cell Based Screening

FILE REFERENCE: 97 022,11

CURRENT APPLICATION NUMBER: US/09/513,783A

CURRENT FILING DATE: 2000-02-25

NUMBER OF SEQ ID NOS: 140

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 100

LENGTH: 4

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Granzyme B

US-09-513-783A-100

Query Match  
Best Local Similarity 66.7%, Score 14, DB 4, Length 4,  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 LEP 4

DB 1 LEP 3

## RESULT 13

US-08-441-871-28

Sequence 28, Application US/08441871

Patent No. 5846765

## GENERAL INFORMATION:

APPLICANT: Matthews, David J.

APPLICANT: Wells, James A.

APPLICANT: Zoller, Mark J.

TITLE OF INVENTION: Identification of No. 5846765-1 Substrates

NUMBER OF SEQUENCES: 152

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIF: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kt floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,871

FILING DATE: 16-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/418928

FILING DATE: 05-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/161692

FILING DATE: 03-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/864452

FILING DATE: 06-APR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US91/09133

FILING DATE: 03-DEC-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/743614

FILING DATE: 09-AUG-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/715300

FILING DATE: 14-JUN-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/683400

FILING DATE: 10-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/621667

FILING DATE: 03-DEC-1990

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Daryl B.

REGISTRATION NUMBER: 32,617

REFERENCE/DOCKET NUMBER: 645902D1

TELEPHONE: 415/225 1249

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-441-871-28

Query Match  
Best Local Similarity 66.7%, Score 13, DB 2, Length 4;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 LEP 4

DB 2 LDP 4

```

RESULT 14
US-09-330-970-16
; Sequence 34, Application US/09330970
; Patent No. 6146876
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: White, David
; TITLE OF INVENTION: A Nucleotide
; TITLE OF INVENTION: Phosphodiesterase
; FILE REFERENCE: 5800-28
; CURRENT APPLICATION NUMBER: US/09/330,970
; CURRENT FILING DATE: 1999-06-11
; EARLIER APPLICATION NUMBER: 09/277,423
; EARLIER FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-330-970-16

```

```

Query Match 65.0%; Score 13; DB 4; Length 4;
Best Local Similarity 100.0%; Pred No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 VLE 3
Db 2 VLE 4

```

```

RESULT 15
US-09-330-970-34
; Sequence 34, Application US/09330970
; Patent No. 6146876
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: White, David
; TITLE OF INVENTION: A Nucleotide
; TITLE OF INVENTION: Phosphodiesterase
; FILE REFERENCE: 5800-28
; CURRENT APPLICATION NUMBER: US/09/330,970
; CURRENT FILING DATE: 1999-06-11
; EARLIER APPLICATION NUMBER: 09/277,423
; EARLIER FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-330-970-34

```

```

Query Match 65.0%; Score 13; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 VLE 3
Db 2 VLE 4

```

```

RESULT 16
US-09-859-242-31
; Sequence 31, Application US/08859242C
; Patent No. 6159938
; GENERAL INFORMATION:
; APPLICANT: Sartech, Inc
; APPLICANT: Albert C. Gyorkos
; APPLICANT: Lyle W. Spruce

```

```

; APPLICANT: Axel H. Leimer
; APPLICANT: John C. Cheronis
; TITLE OF INVENTION: Serine Protease Inhibitors Comprising
; TITLE OF INVENTION: Alpha-Peto Heterocycles
; FILE REFERENCE: 361236 006 (21 CIP)
; CURRENT APPLICATION NUMBER: US/09/859,242C
; CURRENT FILING DATE: 1997-05-20
; EARLIER APPLICATION NUMBER: US 08/345,820
; EARLIER FILING DATE: 1996-11-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Serine Protease
US-09-859-242-31

```

```

Query Match 65.0%; Score 13; DB 4; Length 4;
Best Local Similarity 100.0%; Pred No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 VLE 3
Db 1 VLE 3

```

```

RESULT 17
US-09-357-952-27
; Sequence 27, Application US/09357952
; Patent No. 6248904
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A
; APPLICANT: Yang, Wu

```

```

; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole-Cell
; TITLE OF INVENTION: Fluorescence Screening Assays for Cuspages, Peptidases, Proteases
; TITLE OF INVENTION: Other Enzymes and the Use Thereof
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/09/357,952
; CURRENT FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: US 09/093,642
; EARLIER FILING DATE: 91-JUL-1998
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patent In Ver 2.0
; SEQ ID NO 27
; LENGTH: 4
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-357-952-27

```

```

Query Match 65.0%; Score 13; DB 4; Length 4;
Best Local Similarity 66.7%; Pred No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 LEP 4
Db 1 VEP 3

```

```

RESULT 18
US-09-521-650-27
; Sequence 27, Application US/09521650
; Patent No. 6335429
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han Zhong

```